RESULT 6

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Dev. Dyn. 225:384-391(2002).
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Best Local Similarity 100...
6; Conservative
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SEQUENCE FROM N.A.
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                                                          rissum=Whole;
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SO ON THE SET OF SET OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atakawa T., Aningawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Atakawa T., Aningawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Anakawa T., Hara A., Fukunishi Y., Komo H., Adachi J., Fukuda S., Anakawa T., Hara A., Nishi K., Kiyosawa H., Komo S., Yamanaka I., Asaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., A Adota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T., Ashburner M., Batalov S., Casvant T., Andria M., Batalov S., Casvant T., A Kidota K., Matsuda H.A., Ashburner M., Batalov S., Casvant T., A Schrim D.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T., Ranga N., Andria M., Wagner L., Washio T., Barki K., Tomita M., Aono H., Baldarelli R., Barsh G., A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., A Brownstein M.J., Bult C., Fleccher C., Fujita M., Gariboldi M., Brownstein M.J., Bult C., Fleccher C., Fujita M., Cariboldi M., Loyon P., Maring B., Ringwald M., Rodriguez I., Sakamoto N., Assaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Haysshizaki Y., Soshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q7SYQ6;
Q7SYQ6;
Q1-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Example Affican clawed frog).
Macazoa, GAfrican Clawed Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; ARCOFS33; BABZ5094.1;
GO; GO:0005199; F:BRICCHIAI molecule activity; IEA.
GO; GO:0005198; F:BRICCHIAI molecule activity; IEA.
InterPro; IPRO0535; MSP domain.
InterPro; IPRO0852; PapD-like.
FEAN; PPO0635; MSP domain. 1.
PROSITE; PS5522; MSP; 1.
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
1810018L05R1k protein.
1810018L05R1k.
                                                                                                                                                                                                                       214 AA.
                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-Pancreas;
MEDLINE-21085660; PubMed-11217851;
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                                                                                                                                                                                                                           PRELIMINARY;
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Best Local Similarity
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                                                                    155 SSGPSL 160
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             1 SSGPSL 6
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TISSUE-Moble;

XI TISSUE-MOBLE
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 24, Last annotation update)
01-UMN-2003 (TrEMBLrel. 24, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=98403884; PubMed=9734815;
Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyajima N.,
MEDLINE=22341132; PubMed=12454917;
Kidein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                               "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 215;
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC054306; DrotAlf3306.1; -.
Hypothetical protAlf36.1; -.
SEQUENCE 215 AA; 24274 MW; 16B308E7E754F456 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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100.0%; Pred. No. 1.2e+02;
tive 0; Mismatches 0;
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us-09-848-834a-6.open.rspt

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Brucella melitensis.
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                                                                                                                                                                                                                                                        1 SSGPSL 6
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Q8YJL9
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Q9L913
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STRANFECC 1551 / Obtkosh;
STRANFECC 1551 / Shland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
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                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AR06969; AAK45022.1; TIGR; MT0781; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

TISSUB-Skin;

Strausberg R.;

Strausberg R.;

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC039152; AAH39152.1; --

EMBL; BC039152; AAH39152.1; --

EMBL; BC039157; F:DNA binding; IEA.

GO; GO:0003577; F:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR003650; Oxange.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Actinomacteria, Actinobacteridae, Actinomycetales, Corynebacterineae, Mycobacteriae, Mycobacterium.
                                                                                        Query Match
Best Local Similarity 100.0%; Score 29; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels C
DNA Res. 5:203-216(1998).
EMBL; AB013390; BAB08457.1; -.
SEQUENCE 226 AA; 25019 MW; D833300F9185B978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 257 AA; 25997 MW; 36D9A9AC973C5D54 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to hairy homolog (Drosophila).
                                                                                                                                                                                                                                                                                                                                                                     QUYEES, (TEMBLEE]. 20, Created)
01-MAR-2002 (TEMBLEE]. 20, Last sequence update)
01-MCR-2002 (TEMBLEE]. 20, Last sequence update)
Hypothetical protein MT0781.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                 196 SSGPSL 201
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Matches 6; Conserv
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SEQUENCE FROM N.A.
STRAIN=16M / ATCC 21456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pranck I.T., Chang B.J., Mee B.J., Collignon P.J., Keese P.K.;
"An adherion defective mutant of Aeromonas veronii biovar sobria
associated with copper tolerance.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF187849, AAF32270.1; -
InterPro; IPRO07939; Cop8.
Pfan; PPO5275; Cop8; 32401 MW; 69E414EEB3D8F148 CRC64;
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Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
Aeromonadaceae; Aeromonas.
NCBI_TaxIb=114517;
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Brucellaceae, Brucella.
NCBI_TaxID=29459,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 29; DB 2; Length 284; 100.0%; Pred. No. 1.7e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                       Length 277;
SWART; SM00353; HLH; 1.
SWART; SM00511; ORANGE; 1.
PROSITE; PS00038; HLH 1; 1.
PROSITE; PS50088; HLH 2; 1.
SEQUENCE 277 AA; 29271 MW; FD1B22170CB38338 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical membrane spanning protein BMEI0063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9L913;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annocation update)
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100.0%; Pred. No. 1.6e+02;
ive 0; Mismatches 0;
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Matches 6; Conservative
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100.0%; Score 29; DB 10; Length 392; 100.0%; Pred. No. 2.3e+02; ative 0; Mismatches 0; Indels 0 Query Match Best Local Similarity 100.0 Lage 6; Conservative

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Gaps

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1 SSGPSL 6 엄

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60 SSGPSL 65

PRELIMINARY; RESULT 15 Q8N4F2 ID Q8N4F2 AC Q8N4F2;

01-OCT-2002 (TrEMBLrel. 22, Created) 01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) SOCO SE REPERENT SOCO SE PAR R

NCBI_TaxID=9606

Query Match
100.0%; Score 29; DB 4; Length 35
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels

9 TSADSS I

Search completed: March 10, 2004, 09:25:29 Job time: 8.92996 secs

us-09-848-834a-6.open.rspt

Gaps ö 100.0%; Score 29; DB 16; Length 348; Similarity 100.0%; Pred. No. 2e+02; 6; Conservative 0; Mismatches 0; Indels 0 Brucella melitensia.", Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
PIRI, AB3260, AB3261.
InterPro. 1PR008964; Invasin_intimin.
Hypothetical protein; Complete proceome.
SEQUENCE 348 AA; 36254 MW; 288E042DA7B177AA CRC64; Query Match Best Local Similarity Matches 6; Conserv 1 SSGPSL 6 ò

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RESULT 13 Q7U3U5

140 SSGPSL 145

Q7U3U5 PRELIMINARY, PRT, 358 AA.
Q7U3U5,
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Aminotransferases class-I (EC 2.6.1.9).
HISC/COBC ON SYNW2334.
Synechococcus sp. (Strain WH8102).
Bacteria, Cyanobacteria, Chrococcales, Synechococcus.

NCBI_TaxID=84588;

SEQUENCE FROM N.A.

MEDLINE=22225697; PubMed=12917641;
Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P., Lameddin J., Regala W., Allen B.E., McCarren J., Paulsen I., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
"The genome of a motile marine Synechococcus.";
Nature 424:1037-1042(2003).

Length 358; EMBL; BX569695; CAE08849.1; -. Aminotransferase; Complete proteome. SEQUENCE 358 AA; 40325 MW; 0C353C403E54DC7F CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; 92 SSGPSL 97 1 SSGPSL 6 ઠે

RESULT 14 Q7XK21

Last sequence update) 392 AA Created) Q7XK21; 01-0CT-2003 (TrEMBLrel. 25, Cr 01-0CT-2003 (TrEMBLrel. 25, La 01-0CT-2003 (TrEMBLrel. 25, La OSJNBa0044K18.24 protein. PRELIMINARY; Q7XK21

Oryza sativa (Rice). Wkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Enrhartoideae, Oryzeae, Oryza. NCBI_TaxID=4530; Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia G., Wang S.Y., Ren S.Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheo Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q., Chen L., Fan D.L., Weng Q.J., Zhang L. Lu Y.C., Yu S.L., Liu Y.L., Chen L., Fan D.L., Weng Q.J., Zhang L. Lu Y.C., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,

Zhou B., Chen Z.H., Hao P., Zhang L., Wu

Σ.

Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L. Zhang R.Q., Guan J.P., Hong G.F.;
Zhang R.Q., Guan J.P., Hong G.F.;
Submitred (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ALEOSESSE; CAROS882.1;
SEQUENCE 392 AA; 42199 MW; 4C7982796D01576F CRC64;

395 AA

LOCIGSIOO. Homo sapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo

[1] SEQUENCE FROM N.A.

TISGUE-Brain;
Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034405; AAH34405.1; -.
SEQUENCE 395 AA; 41599 MW; E9E4D81DEF45D414 CRC64;

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323 SSGPSL 328

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Gaps

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144 SSGPSL 149
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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BATS_HUMAN
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MYCD RAT
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KCH7_HUMAN
CTC_EUGGR
HIA_XENLA
YUBG_CAEEL
CXC_EUGGR
HIA_XENLA
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1 SSGPSL 6
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NIFE RHISN YM43 YEAST NU62_HUMAN PRAIL_COREF PEPA_FUSINN HILZ_ARATH HEPA_BACTN GSPD_XANCP AVP3_HORVU AVP3_PHAAU AVP3_PHAAU AVP3_ARATH RINI_RAT RINI_RAT	DARD; PRT; 225 AA. 9, Created) 9, Last sequence update) in V. tive-strand viruses; Monon ramyxovirinae; Rubulavirus AND RNA EDITING. AND RNA EDITING. AND RNA EDITING. AND FRA EDITING. AND	NYX_P_V. V; 1. A editing. CYS-RICH. MW; 1A749260CAB7D71E C 0%; SCORE 29; DB 1; I 0%; Pred. No. 29; 0; Mismatches 0;
55105 5105 5105 5105 5105 5105 5105 510	STANDARD; PRT; 4 (Rel. 29, Created) 4 (Rel. 29, Last sequence tal protein V. SRA, negative-strand virus ridae; Paramyxovirinae; Ru 11228; ROM N.A., AND RNA EDITING. Miba/Chanok; Getorination of the p ger deletions near the RNA-edi TRUNGS MOdified positions g at this position consist indee. The sequence displace the unedited RNA. The edite 6606). RITY: TO THE V PROTEIN OF FIGURE INSTITUTE OF BIOM AND THE SALES INSTITUTIONS AS AND THE SALES INSTITUTIONS AS AND THE SALES ASSALES ASSALES.	0. 7; Parai amyx P. 221 221 24048 100. 100. vative
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264 SSGPSL 269
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"Human Sir2-related protein SIRT1 associates with the bHLH repressors
HES1 and HES2 and is involved in HES1- and HEY2-mediated
transcriptional repression.";
Biochem. Biophys. Res. Commun. 301:250-257(2003).
-!- FUNCTION: Transcriptional repressor of genes that require a bHLH
protein for their transcription. May act as a negative regulator of myogenesis by inhibiting the functions of MYOD1 and ASH1 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -u-suminativy...

SUBBURIT: Transcription repression requires formation of a complex with a co-repressor protein (Groucho) such as TLE2 (By similarity). Interacts with SIRTI.

SUBCELLULAR LOCATION: Nuclear.

-i- DOMAIN: Has a particular type of basic domain (presence of a helix-interrupting proline) that binds to the N-box (GACNAG), rather than the canonical B-box (GANNTG).

-i- DOMAIN: The carboxyl-terminal WRPW motif is a transcriptional repression domain necessary for the interaction with GROUCHO, a transcriptional co-repressor recruited to specific target DNA by HAIRY-related proteins.

-i- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Makamura Y., Isogani T., Sugano S., Isogani T., Subanitted (FEB-2000) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                   IS-DEC-1998 (Rel. 37, Created)
IS-DEC-1998 (Rel. 37, Lact sequence update)
IS-MAR-2004 (Rel. 37, Lact annotation update)
Transcription factor HES-1 (Hairy and enhancer of split 1) (Hairy-HIS) (HHL) (Hairy homolog).
Hike) (HHL) (Hairy homolog).
Homo sapiens (Human).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feder J.N., Li L., Jan L.Y., Jan Y.-N.; "Reder J.N., Li L., Jan L.Y., Jan Y.-N.; "Genomic cloning and chromosomal localization of HRY, the human homolog to the Drosophila segmentation gene, hairy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Year J. Yeung S., Sun H., Chen N.;
"Functional analysis of human HRY in Drosophila.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                      280 AA
                                                      PRT;
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INTERACTION WITH SIRT1.
MEDLINE=22422590; PubMed=12535671;
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MEDLINE=94292187; PubMed=8020957;
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EMBL, AK0004015, BAA91149.1; --
PIR, A53027, A53027
TRANSFAC, T04892;
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                                                            STANDARD;
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Genew; HGNC:5192; HES1

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STRAIN=Toshiba/Chanock,
MEDILINE-32560408; PubMed=8492098;
Kawano M., Tsurudome M., Oki N., Nishio M., Komada H., Matsumura H.,
Kusaqawa S., Ohta H., Ito Y.,
Kusaqawa S., Ohta H., Ito Y.,
"Sequence determination of the P gene of simian virus 41: presence of
irregular deletions near the RNA-editing sites of paramyxoviruses.";
J. Gen. Virlo. 74:311-916 (1939).
-1. FUNCTION: Essential component of the RNA polymerase and the
nascent chain assembly complex. Also required during RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - RNA DITING: Modified positions=164; Note=Partially edited. RNA editing at this position consists of an insertion of two guanine nucleotides. The sequence displayed here is the P protein, derived from the edited RNA. The unedited RNA version gives rise to the V protein (AC P36315).
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caralytic ACTIVITY: N nucleoside triphosphate = N diphosphate
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SER/THR-RICH.
WRPW MOTIF (REQUIRED FOR ACTIVITY)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 29; DB 1; Length 280; 100.0%; Pred. No. 37; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA negative strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF03210; Paramyx P V; l. Transferase; Nucleocapsid;
Transferase; RNA-directed RNA polymerase; Nucleocapsid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-WAR-2004 (Rel. 43, Created)
15-WAR-2004 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
RNA polymerase alpha subunit (BC 2.7.7.48) (P protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F9342A88FC749E3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S60813; AAB26640.2; -.
PIR; JQ2041; JQ2041.
InterPro; IPR004897; Paramyx P.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 AA; 29541 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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1 SSGPSI 6
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NON TER
SEQUENCE
                                                                                                             NAP5 HT
014513
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                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20144096; PubMed=10677514;
MEDLINE=20144096; PubMed=10677514;

Kim C.B., Amemiya C., Balley W., Kawasaki K., Mezey J., Miller W.,

Kim C.B., Amemiya C., Balley W., Kawasaki K., Mezey J., Miller W.,

Minoshima S., Shimizu N., Wagner G., Ruddle F.;

"Hox cluster genomics in the horn shark, Heterodontus francisci.";

Proc. Natl. Acad. Sci. U.S.A. 97:1655-1660(2000).

-!- FUNCTION: Sequence-specific transcription factor which is part of
a developmental regulatory system that provides cells with
specific positional identities on the anterior-posterior axis (By
                                                                     Gaps
                                                                                                                                                                                                                                                                                       Heterodontus francisci (Horn shark).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
Heterodontidae; Heterodontus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02833; 15AN.

R TRANSFAC; T04474; -.

R InterPro; 1PR001827; Homeobox; 1.

R InterPro; 1PR001827; Homeobox; 1.

R PRINTS; PR00024; MYENNAPEDIA.

R PRINTS; PR00024; HOMEOBOX; 1.

R PRINTS; PR00024; HOMEOBOX; 1.

R SWART; SM0389; HOX; 1.

R PROSITE; PS00037; HOMEOBOX 1:

R PROSITE; PS0071; HOMEOBOX 2; 1.

R PROSITE; PS0071; HOMEOBOX 2; 1.

R HOMEOBOX; DNA-binding; Developmental protein; Nuclear protein; I Tanscription regulation.

R Transcription regulation.

R SITE
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                                       100.0%; Score 29; DB 1; Length 395; 100.0%; Pred. No. 52; cive 0; Mismatches 0; Indels
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POLY-GIN.
POLY-PRO.
POLY-SER.
285ABC06B41C9FD9 CRC64;
Phosphorylation, RNA editing.
SEQUENCE 395 AA; 41920 MW; 6E97477FBF483D30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the Antp homeobox family.
                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF224262; AAF44641.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44548 MW;
                                                                     Conservative
                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                 Homeobox protein Hox-A3.
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410 AA;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                          144 SSGPSL 149
                                                      Local Similarity
les 6; Conserv
                                                                                              SSGPSL 6
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein Nck.
-1- TISSUE SPECIFICITY: Expressed in fetal and adult brain, leukocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98008866; PubMed=9344857;
Matuoka K., Miki H., Takahashi K., Takenawa T.;
Matuoka K., Miki H., Takahashi K., Takenawa T.;
Matuoka I.;
Matuoka 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=74-0R23-1A / FGSC 987;
STRAIN=74-0R23-1A / FGSC 987;
STRAIN=74-0R23-1A / FGSC 987;
Aronson B.D., Johnson K.A., Dunlap J.C.;
"Circadian clock locus frequency: protein encoded by a single open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 29; DB 1; Length 416; 100.0%; Pred. No. 55;
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                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
29-FEB-2003 (Rel. 41, Last annotation update)
Nck-associated protein 5 (NAP-5) (Fragment).
                                                                                                                                                                                                                                      416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Best Local Similarity luv...
6; Conservative
                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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346 SSGPSL 351
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Gaps

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Gaps

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Conservative

15-UUL-1999 (Rel. 38, Created) 15-UUL-1999 (Rel. 38, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Frequency clock protein.

Sordaria fimicola.

997 A.A.

STANDARD;

FRQ SORFI ID FRQ SORFI AC Q09033;

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MEDLINE=21956574; PubMed=1959847;

RA MEDLINE=21956574; PubMed=1959847;

RA MEDLINE=21956574; PubMed=1959847;

RA MEDLINE=21956574; PubMed=1959847;

RA MEDLINE=21956574; PubMed=1959847;

RT "Requiation of the Neurospora circadian clock by casein kinase II.";

Genes Dev. 16:994-1006(2002).

-!- FUNCTION: Circadian clock component involved in the generation of langth, and temperature compensation. Oscillates in abundance with a daily peak early in the morning. Behaves as a negative element of in circadian transcriptional loop. May bind to wc2 protein. The complex frq wc2 may turn off the expression of frq.

-!- ALTERNATIVE PRODUCTS:

COMMENTE-2 isoforms. Long (8hown here) and Short, are produced by alternative initiation. The isoform Long maintains rhythms at lower temperature (18 degrees Celaius);

-!- INDUCTION: By light; perhaps through white collar-1 (wc1) and maintains rhythms at lower temperature (18 degrees Celaius);

-!- Thy representive phosphorylation is also involved in regulating frq degradation. Phosphorylation is also involved in regulating frg degradation. Phosphorylation is also involved in regulating frg degradation. Phosphorylation between frg and the white collar proteins, and complex formation between frg and the white collar proteins, and read-hark long.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR ISOFORM SHORT.
POLY-SER.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biological rhythms; Transcription regulation; Nuclear protein;
Phosphorylation; Alternative initiation.
CHAIN 10989 FREQUENCY CLOCK PROTEIN, ISOFORM LONG.
CHAIN 100 989 FREQUENCY CLOCK PROTEIN, ISOFORM SHORT.
                                                             SECUENCE OF 202-989 FROM N.A.
MEDLINE-89281721; PubMed-2525233;
McClung C.R., Fox B.A., Dunlap J.C.;
The Neurospora clock gene frequency shares a sequence element with the Drosophila clock gene period.";
Nature 339:558-562(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E-SK: IN FRQ3, LENGTHENED PERIOD.
G-SD: IN FRQ3, LENGTHENED PERIOD.
G-SS: IN FRQ1, SHORTENED PERIOD.
MISSING: IN FRQ9, LOSS OF RHYTHMICITY.
A-YI: IN FRQ9, SHORTENED PERIOD.
EATLRH -> MGGNRP (IN REF. 2).
Y -> H (IN REF. 2).
reading frame defines period length and temperature compensation.", proc. Natl. Acad. Sci. U.S.A. 91:7683-7687(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 Y -> H (IN REF. 2).
108229 MW; 79E2A353E6A8099F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE FRO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U17073; AAA57121.1; -. PIR; T46659; T46659. Biological rhythms; Transcrip
                                                                                                                                                                                                                   PHOSPHORYLATION BY CK2
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663
895
202
233
233
AA;
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DOMAIN
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MUTAGEN
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CONFLICT
SEQUENCE
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Campbell J.B., Zhao Y.;
Camptell J.B., Zhao Y.;
Submitted (AUG-1996) to the EMEL/GenBank/DDBJ databases.
Submitted (AUG-1996) to the EMEL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          + {DNA}(N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Intergeneric complementation of a circadian rhythmicity defect: phylogenetic conservation of structure and function of the clock gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN 868 894 ASP/GLU-RICH (ACIDEC) BOMAIN 868 894 ASP/GLU-RICH (ACIDEC).
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Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i. FUNCTION: Circadian clock component involved in the generation biological rhythms, in particular in rhythm stability, period length, and temperature compensation. Behaves as a negative element in circadian transcriptional loop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                           Eukaryora; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Sordaria.
NCBI_TaxID=27338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 29; DB 1; Length 997; 100.0%; Pred. No. 1.4e+02; tive 0; Mismatches 0; Indels
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1149 AA.
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FGSC 2918;
MEDLINE=94252311; PubMed=8194516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L14467; AAA20825.1; -. PIR; S44457; S44457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frequency.";
EMBO J. 13:2257-2266(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 SSGPSL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merrow M.W., Dunlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SSGPSL 6
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q65946;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Length 989; Indels

Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0;

271 SSGPSL 276 SSGPSL 6

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Pred. No. 1.6e+02; Mismatches 0; Mismatches

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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bicinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: This DNA polymerase requires a protein as a primer. -!- SIMILARITY: Belongs to the DNA polymerase type-B family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canine adenovirus type 2 (strain Toronto A 26-61).
Viruses, dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
NCBI_TaxID=69152;
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          SIMILARITY: Belongs to the DNA polymerase type-B family.
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Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00116; DNA POLYMERASE B; 1.
Transferase, DNA-directed DNA polymerase; DNA replication;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1149 AA; 130939 MW; AOB686FAEFFA236E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA polymerase (EC 2.7.7.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1150 AA.
                                                                                                                                                                                                                                                                                                                                EMBL, U55001, AAB05434.1; InterPro; IPR006417; DNA pol B.
InterPro; IPR004868; DNA pol B.2.
InterPro; IPR004137; Prismane.
Ffam; PP03175; DNA pol B.2; 1.
PRINTS; PR00106; DNAPOLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U77082; AAB38716.1; -: InterPro; IPR006172; DNA_pol_B. InterPro; IPR004868; DNA_pol_B_Z. InterPro; IPR004137; Prismane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF03175; DNA pol B 2; 1.
PRINTS; PR00106; DNAPOLB.
SMART; SM00486; POLBC; 1.
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ID DPOL ADECT
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Matches
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Length 1150;

DB 1;

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=2154388; PubMed=11707778;
Brown S. E., Campbell R.D., Sanderson C.M.;
"Novel NG36/G9a gene products encoded within the human and mouse MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Salivary gland;
Oshima A., Takahashi-Fulii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saitor K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma I
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahit K., Masuho Y., Nagai K., Isogai T.;
Submitted (OCT-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks
Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.,
"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Hirakawa M., Yamaguchi H., Imai K., Shimada J., Shiina S., Tamiya
Oka A., Inoko H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                            STANDARD, PRT; 1210 AA.

Q96KQT; Q14349; Q96MB; Q96QD0; Q9QL0; Q9Y331;
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Histone-1ysine N-methyltransferase, H3 Lysine-9 specific 3 (EC 2.1.1.43) (Histone H3-K9-methyltransferase 3) (H3-K9-HMTase 1 HIA-B associated transcript 8) (G9a) (NG36).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 5-1210 FROM N.A. (ISOFORM 1).
100.08; FE.
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                                                                                                                                                                     25 SSGPSL 30
                                                                                                            1 SSGPSL 6
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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PROSITE; PS50088; ANK REPEAT; 5.
PROSITE; PS50297; ANK REP REGION; 1.
PROSITE; PS50868; POST SET; PALSE_NEG.
PROSITE; PS50280; SET; 1.
PROSITE; PS50280; SET; 1.
Transferame; Methyltransferame; Chromatin regulator; Nuclear protein;
Transferame; Methyltransferame; POLY-ALA.
DOMAIN
2 13
POLY-ALA.
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PTIGL4VBP 002211.
PPUREXEP -> VSGMGEMG (in isoform 3)
FPIIG-VSP_002212.
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/FIId=VSP 002213.

A -> Q (IN REF. 5; AAH18718).

A -> G (IN REF. 5; AAH20970).

N -> T (IN REF. 1 AND 4).

PP -> TR (IN REF. 2; AAH02686).

C -> R (IN REF. 3).

C -> R (IN REF. 3).
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POLY-GLU.
ANK 1.
ANK 3.
ANK 3.
ANK 5.
ANK 6.
ANK 6.
ANK 7.
PRE-SET.
POST-SET.
                                                                                                                                                                                                                                                                             EMBL; AP000502; BAB63295.1; ALT_SEQ.
EMBL; AJ315532; CAC86666.1;
EMBL; BC05686; BAB1314.1;
EMBL; BC002686; AAH02686.1; ALT_INIT.
EMBL; BC018718; AAH18718.1; ALT_INIT.
EMBL; BC020970; AAH20970.1; ALT_INIT.
EMBL; K69838; CAA44491.1; ALT_INIT.
                                                                                                                                                                                          EMBL; AF134726; AAD21811.1; ALT_SEG.
EMBL; AF144726; AAD21812.1; ALT_SEG.
EMBL; AP000502; BAB63294.1; ALT_SEG.
EMBL; AP000502; BAB63295.1; ALT_SEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001214; SET.
InterPro; IPR001214; SET.
InterPro; IPR003606; Zn2-binding.
Pfam; PP00023; Pre-SET; 1.
Pfam; PP00866; SET; 1.
PRINTS; PR01415; ANXYRIN.
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InterPro; IPR003616; POSTSET.
InterPro; IPR007728; Pre-SET.
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SMART; SM00468; PreSET; 1.
SMART; SM00317; SET; 1.
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC
MIM; 604599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DENTIFICATION IN COMPLEX WITH E2F6; TFDP1; MAX; MGA; EUHMTASE1; CBX3; RING1; RNF2; MBLR; L3MBTL2 AND YAF2.

REMUG1: RNF2; MBLR; L3MBTL2 AND YAF2.

REMUG1: RNF2; MBLR; L3MBTL2 AND YAF2.

REMUG1: Tablique K.-I., Gaubatz S., Livingston D.M., Nakatani Y.; A ogawa H., Ishiguro K.-I., Gaubatz S., Livingston D.M., Nakatani Y.; A complex with chromatin modifiers that occupies E2F- and Wyc-responsive genes in GO cells."; Schoce 295:1132-1136(2002).

Refunction Histone methyltransferase. Preferentially methylates

Lyg-9 of histone H3 and Lyg-27 of histone H3 (in vitro): H3 Lyg-9 of histone H3 and Lyg-7 of histone H9 proteins to methylation represent a specific tag for epigenetic reanscriptional repression by recruiting HP1 proteins to methylated histones. Probably targeted to histone H3 by different methylated histone H1 (By similarity).

C. - CATALYTIC ACTIVITY: S-adenosyl-L-methionine + histone L-lysine = S-adenosyl-L-homocysteine + histone L-lysine.

S. - CATALYTIC ACTIVITY: S-adenosyl-L-methionine + histone L-lysine = S-adenosyl-L-homocysteine + histone L-lysine.

S. - CATALYTIC ACTIVITY: S-adenosyl-L-methionine + histone L-lysine.

S. - CATALYTIC ACTIVITY: S-adenosyl-L-methionine + histone L-lysine.

S. - CATALYTIC ACTIVITY: S-adenosyl-L-methionine + histone L-lysine.

S. - CATALYTIC ACTIVITY: S-adenosyl-L-methonine.

S. - CATALYTIC ACTIVITY: S-adenosyl-L-methonine.

C. - SUBDNIT: Part of the E2P6. com-1 complex in G0 phase composed of E2F6, MGA, MAX TFDP1, CBX3, BAT8, EUHMTASE1, RING1, RNF2, MBLR, CC-1-SUBCELLUMAR LOCATION: Nuclear; associates with euchromatic regions. Does not associate with heterochromatin.

C. - ALTERNATIVE ROOUCTER.

FRANCE CATALYTIC ACTIVITY: Nuclear, index 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Sold=096K07-1; Sequence=Displayed; | Name=2; Synonyms=NG36G9a-SPI; | Name=2; Synonyms=NG36G9a-SPI; | Name=2; Synonyms=NG36G9a-SPI; | Name=2; Synonyms=NG36; | Squence=VSP_002213; | Name=3; Synonyms=NG36; | Squence=VSP_002212; | VSP_002213; | Name=3; Synonyms=NG36; | Name=3; Sanonyms=NG36; | Name=3; Name=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGYMATIC ACTIVITY, AND SUBCELLULAR LOCATION.

MEDLINE-21326082; PubMed=11316813;

Tachibana M., Sugimoto K., Fukushima T., Shinkai Y.;

"Set domain-containing protein, G9a, is a novel lysine-preferring mammalian histone methyltransferase with hyperactivity and specific selectivity to lysines 9 and 27 of histone H3.";

[8]
                                                                                                                                                                                                                                                                                                    TISSUE=Histiocytic lymphoma;
MEDLINE=93207535; PubMed=8457211;
Milher C.M., Campbell R.D.;
"The G9a gene in the human major histocompatibility complex encodes novel protein containing ankyrin-like repeats.";
Blochem. J. 290:811-818(1993).
                   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones B.J.W., Marra M.A.; Generation and intial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                       SEQUENCE OF 195-1210 FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event-Alternative splicing, Named isoforms=3;
Comment-Additional isoforms seem to exist;
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Gaps

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Indels

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605

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methionine.

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TISSUE=Breast tumor;

X Statesberg F. D. Facon N.A.

TISSUE=Breast tumor;

MEDLINE=22388257; PubMed=12477932;

X Statesberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Bronstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley A.M., Schergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

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Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)

Rubman and mouse colNA sequences "S. M., Mara M.A.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE SPLICING (ISOFORM 2).
MEDLINE-21184388; PubMed=11707778;
MEDLINE-211859 PubMed=11707778;
Brown S.E., Campbell K., Sanderson C.M.;
"Novel NG36/G9a gene products encoded within the human and mouse MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1165-ASN--CYS-1168.
MEDLINE=22123403; PubMed=12130538;
MEDLINE=22123403; PubMed=12130538;
Machibana M., Sagmoto K., Nozaki M., Ueda J., Ohta T., Ohki M., Fukuda M., Takeda N., Niida H., Kato H., Shinkai Y.;
"G9a histone methyltransferase plays a dominant role in euchromatic histone H3 lygine 9 methylation and is essential for early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R., Schaffer T., Ratciliffe A., Abbasi N., Loretz C., Lasky S., Hood L.; "Sequence of the mouse MHC class III region."; Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                DATA MOUSE STANDARD; PRT; 1263 AA.

O92148; OBK4R6; OBK4R7; O32149;
D92148; OBK6R6; OBK4R7; O32149;
28-FFB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Histone-lysine N-methyltransferase, H3 lysine-9 specific 3
Histone-lysine N-methyltransferase, H3 lysine-9 specific 3
(HLA B associated transcript 8) (G9a) (NG36).
BAT8 OR G9A OR NG36.
                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND MUTAGENESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes Dev. 16:1779-1791(2002).
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Mamm. Genome 12:916-924(2001),
                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    embryogenesis."
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STRAIN=129;
                                                                                                                    CRITICE STATES SEED TO SEED TO
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Event_Alternative splicing; Named isoforms=2;

Event_Alternative splicing; Named isoforms=2;

Name=1; Synonyms=G9a-L;

Isoid=Q92148-1; Sequence=VSP 002214, VSP 002215, VSP 002216;

Isoid=Q92148-2; Sequence=VSP 002214, VSP 002216;

Isoid=Q92148-2; Sequence=VSP 002214, VSP 002216;

ISOIMIARITY: Belongs to the histone-lysine methyltransferase family. Suvara-3 subfamily.

ISINILARITY: Contains 7 ANK repeats.

ISINILARITY: Contains 1 Dre-SET domain.

ISINILARITY: Contains 1 Dre-SET domain.

ISINILARITY: Contains 1 Dost-SET domain.
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SMART; SM00248; PreSET; 1.
SMART; SM00468; PreSET; 1.
SMART; SM00317; SFT; 1.
PROSITE; PS50089; ANK REPEAT; 5.
PROSITE; PS50869; POST SFT; PALSE_NEG.
PROSITE; PS50860; POST SFT; PALSE_NEG.
PROSITE; PS50860; POST SFT; 1.
Transferase; Methyltransferase; Chromatin regulator; Nuclear protein;
Lys-9 of histone H3 and Lys-27 of histone H3 (in vitro). H3 Lys-f methylation represents a specific tag for epigenetic transcriptional represents by recruiting HP1 proteins to methylated histones. Also methylates histone H1.

-! CATALYTIC ACTIVITY: S-adenosyl-L-methionine + histone L-lysine = 3-adenosyl-L-methionine + histone L-lysine = 1-SUBUNIT: Part of the B2F6.com-1 complex in G0 phase composed of E2F6, MGA, MAX, TFDP1, CBX3, BAT8, EUHWTASE1, RING1, RNF2, MBLR, L3MBTL2 and YAF2 (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear; almost excluded form nucleoli.

Associates with euchromatic regions. Does not associate with
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POLY GLU.
ANK 1.
ANK 2.
ANK 3.
ANK 4.
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ANK 6.
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EMBL; AF109906; AAC84164.1; ALT SEQ.
EMBL; AB077210; BAC05482.1;
EMBL; AB07210; BAC05482.1;
EMBL; BC02553.9; AAH2553.1; ---
EMBL; BC02553.9; AAH2553.1; ---
EMBL; BC02553.9; AAH2553.1; ALT_INIT.
INTERPRO; IPR002110; ANK.
INTERPRO; IPR00310; ANK.
INTERPRO; IPR001214; SET.
INTERPRO; IPR001214; SET.
INTERPRO; IPR001214; SET.
INTERPRO; IPR001214; SET.
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Pfam; PP05033; Pre-SET; 1.
Pfam; PP00856; SET; 1.
PRINTS; PR01415; ANKYRIN.
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ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                         DOMAIN
CONFLICT
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                                                                                                                                                         isoform 2).
/FTIG=NSP 002215.
Misding (In isoform 2).
/FTIG=NSP 002216.
R->H: STRONGLY REDUCES HISTONE
MISSING: ABOLISHES ACTIVITY.
MISSING: ABOLISHES HISTONE
MISSING: ABOLISHES HISTONE
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R PIR; 5249627; CAA89658.1; -.

R PIR; 525150, 557150.

R RSP; PO7448; 1ARD.

R TRANSPAC; TO46595; -.

R TRANSPAC; TO46595; -.

R SGD; S000388; ZMI.

R PÉAN; PRO0096; zf.C2H2; 2.

R PAR, SMART; SM0355; ZIR C2H2; 2.

R PROSITE; PS0157; ZINC_FINGER C2H2 1; 2.

R PROSITE; PS0157; ZINC_FINGER C2H2 2; 2.

M DNA-binding; Nuclear protein; Zinc-finger; Metal-binding; Repeat.

T DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                        /FTIG=VSP 002214.
AGLIGPPVPCLPSQ -> MAAAAGAAAAABE (in
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
21nc finger protein ZMS1.
ZMS1 OR VRR127C OR U2052.
ZMS1 OR VRR127C OR U2052.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Asocomycota; Saccharomycetes; Saccharomycestales; Saccharomycestales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1263;
                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 29; DB 1; Length 12:
100.0%; Pred. No. 1.88+02; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=RC11-6A;
Thomas D., Barbey R., Surdin-Kerjan Y.;
Submitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.
                                                                               (in isoform 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1380 AA
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                              SET.
POST-SET.
Missing (
          PRE-SET
                                                                                                                                                                                                                                                                                                                                                                                          1263 AA; 138038 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
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          1025
1090
1217
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                                                                                                                                                                                                                                                                                                                  1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZMS1 YEAST
P46974;
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                       /ARSPLIC
                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                    MUTAGEN
                                                                                                                                                                                                                                                                                                                     MUTAGEN
          DOMAIN
DOMAIN
DOMAIN
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ZMS1_YEAST
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Matches
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TTCKTTAVLVISEYNKCVEDBARGYYRANNFNSALLDFSDRV
INLAGREILERLGMNLIPKECDVLKSYTDFLRWQDKDALDD
SALNEEGAQGRANDPNTDINETIQLIYAASLSSKCLYLGVQI
IQDAPIWPIILSFAHGLQSRAIYSVTKKRNTRI -> S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS 3 AND 4), FUNCTION, ALTERNATIVE PROMOTER USAGE, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTANTS E9 AND
                                                                                                                                NL -> IF (IN REF. 1).
N -> H (IN REF. 1).
RLIIPVYLFAKMRRCLDLAHVIEKIWLKDWSNYMKALEEVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-Endryo;
MEDLINE=20157049; PubMed=10655223;
Rebay I., Chen F., Heiao F., Kolodziej P.A., Kuang B.H., Laverty T., Sub C., Voas M., Williams A., Rubin G.M.;
"A genetic screen for novel components of the Ras/mitogen-activated protein kinase signaling pathway that interact with the yan gene of Drosophila identifies split ends, a new RNA recognition motif-containing protein.";
Genetics 154:695-712(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=20025936; PubMed=10556062;
Wiellette E.L., Harding K.W., Mace K.A., Ronshaugen M.R., Wang F.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "spen encodes an RNP motif protein that interacts with Hox pathways to repress the development of head-like sclerites in the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=2017175; PubMed=10704397; Kuang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej P.A.; Kuang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej P.A.; Explit ends encodes large nuclear proteins that regulate neuronal cell fate and axon extension in the Drosophila embryo."; Development 127:1517-1529(2000).
C2H2-TYPE 1.
C2H2-TYPE 2.
POLY-GAN
MEPFAFGRGAPALCILT -> MHTN (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
SPEN DROME
STANDARD; PRT; 5560 AA.

10 SORNAN; QSNUTJ; QSNUCCJ; QSVPLI; QSVPLZ;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DF Split ends protein.
GN SpEN OR CG18497.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryotzi, Metazozi Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neopiera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophila.
OX NCBI_TAXID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [3]
SEQUENCE FROM N.A. (ISOFORM 1), SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         (IN REF. 1).
1380 AA; 155062 MW; FBE987EA5B639000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 29; DB 1; L
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND TISSUE SPECIFICITY STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Development 126:5373-5385(1999).
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REDLINE=20196006; PubMed=10731132;
Radams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Radams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RAD Amanatides G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutron G.G., Wortman J.R., Yandfall M.D., Zhang Q., Chan. L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Ashburner M., Pfeiffer B.D.,
RAD Erandon R.C., Baxter E.G., Helf G., Nelson C.R., Miklos G.L.G.,
RAD Abril J.E., M., Bennos P.V., Bernam B.P., Bandari D., Bolahakov S.,
Ballew R.M., Bannos P.V., Bernam B.P., Bandari D., Bolahakov S.,
Borkova D., Botcher M.R., Bouck J., Brokstein P., Brottlier P.,
RAD Borkova D., Botcher A., Deug Z., Mays A.D., Dew I., Dietz S.M.,
Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RAD Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Flaischman W.,
RAD Glodek A., Gong F., Gornell J.H., Gu Z., Glaba P., Harris M.,
RAD Harris N.L., Harvey D.A., Heiman T.J., Nel M.-I., Ibegwam C.,
RAD Alali M., Kalush F., Kalyen G.H., Ke Z., Kannison J.A., Kettlem
RAD Alali M., Kalush F., Kalyen G.H., Ke Z., Kannison J.A., Kettlem
RAD Lasko P., Lei Y., Leviteky A.A., Li J.H., Li Z., Lidang Y., Lai Z.,
Lasko P., Lei Y., Leviteky A.A., Li J.H., Li Z., Lidang Y., Lai Z.,
RAD Lasko P., Lei Y., Murphy B., Murphy L., Wanny D.M., Nelson D.L.,
RAD Lasko P., Lei Y., Murphy B., Murphy L., Wanny D.M., Nelson D.L.,
RAD Lasko P., Lei Y., Leviteky A.A., Li J.H., Li Z., Lidang Y., Lin X.,
RAD Lasko P., Lei Y., Murphy B., Murphy L., Wanny D.M., Nelson D.L.,
RAD Lasko P., Lei Y., Murphy B., Murphy L., Wanny D.M., Nelson D.L.,
RAD Lasko P., Lei Y., Marking C.C., Kraft C., McHeber D., Wanny D.M., Nelson D.K., Mirching C.C., Scheeler F., Spradling A.C., Stapleton M., Studger R., Sun E.,
Syliekas R., Woodage T., Worley K.C., Wu D., Yang S., Yang S., Yang S., Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 424-2002 FROM N.A.
STRAIN=Berkeley; TISSUB=Embryo.
MEDLINE=22426066, PubMed=12537569;
Stapleron M., Carlson J.W., Broketein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
Rubin G.M., Celniker S.E.;
"A prosophila full-length CDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A screen for modifiers of cyclin E function in Drosophila melanogaster identifies Cdk2 mutations, revealing the insignificance of putative phosphorylation sites in Cdk2."; Genetics 155:233-244(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELICING, AND ALTERNATIVE SPLICING.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.F.
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Staplecon M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lane M.E., Elend M., Heidmann D., Herr A., Marzodko S., Herzig A., Lehner C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20253107; PubMed=10790398;
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[8]
FUNCTION ON EGF RECEPTOR PATHWAY.
MEDLINE=20414403; PubMed=10959845;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name-4; Synonyme-Spens; Name-4; Synonyme-Spens; Name-4; Synonyme-Spens; Name-4; Synonyme-Spens; Note-Produced by alternative Eplicing of isoform 2; Note-Produced by alternative. Eplicing of isoform 2; TISSUE SPECIFICITY: Ubiquitous. Expressed prior to cellularization in stage 3 embryos, and in blastoderm cells, including pole cells. Expressed throughout the rest of embryogenesis. Later, it is expressed at higher level in epidermal cells and CNS.

DEVELOPMENTAL STAGE: Isoform 3 is expressed both maternally and
                                                                                                                                                                                                      signaling...

Development 130:3125-3135(2003).

Development 130:3125-3135(2003).

Levelopment 130:3125-3135(2003).

Levelopment 130:3125-3135(2003).

Rey pathways such as the EGF receptor and Wg pathways. Involved in neuronal cell fate, survival and axon guidance, cell cycle regulation and repression of head identity in the embryonic trunk. May act with the Hox gaene Deformed and the EGF receptor signaling pathway. Positive regulator of the Wg pathway in larval tissues but not in embryonic tissues. May act as a transcriptional corepressor protein, which repress transcription via the recruitment of large complexes containing histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins.
SUBCELLUAR LOCATION: Nuclear.
ALTERNATIVE PRODUCES:
Event=Alternative promoter;
Comment=2 isoforms, 1 (shown here) and 2, are produced by use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the Spen family.
SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
SIMILARITY: Contains 1 SPOC domain.
CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.
Chen F., Rebay I.;
"split ends, a new component of the Drosophila EGF receptor pathway,
regulates development of midline glial cells.";
Curr. Biol. 10:943-946(2000).
                                                                                                                   FUNCTION ON WG PATHWAY.
MEDLINE-22668876, PubMed=12783785,
Lin H.V., Doroquez D.B., Cho S., Chen F., Rebay I., Cadigan K.M.;
"Splits ends is a tissue/promoter specific regulator of Wingless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=3; Synonyms=SpenL;
IsoId=Q8SX83-3; Sequence=VSP_008567;
Note=Produced by alternative splicing of isoform 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isoid=085x83-2; Sequence=VSP_008565; VSP_008566;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q8SX83-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0007411; P:axon guidance; IMP.
GO; GO:0008347; P:glia cell migration;
Interpro; IRRO00504; RNA_rec_mot.
Pfam: PF00076; rrm; 3.
SMART; SM00360; RRM; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50102; RRM; 3.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF188205, AAF13218.1, -.
EMBL, AF28412; AAF26299.1; -.
EMBL, AF221715, AAF24661.1, ALT_INIT.
EMBL, AE003590; AAF51535.2; -.
EMBL, AE003590; AAF51535.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003590; AAN10511.1; -. EMBL; AY094788; AAM11141.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alternative promoters;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0016977; spen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zygotically.
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TISSUE=EMDAYO.

TISSUE=EMDAYO.

XX MEDINE=20368176; PubMed=10906470;

XX Crociani O., Cherubini A., Piccini E., Polvani S., Costa L.,

A crongali A.;

A reangeli A.;

A reangeli A.;

Bech Dev. 95:239-243(2000).

YE System of quali embryos.";

Mech. Dev. 95:239-243(2000).

YE TUNCIYON: Porce-forming (alpha) subunit of voltage-gated inwardly rectifying potassium channel (By similarity).

C -! FUNCIYON: Porce-forming (alpha) subunit of voltage-gated inwardly rectifying potassium channel is probably composed of a homo-or hore-arcteramento complex of pore-forming alpha subunits that can associate with modulating beta subunits (By similarity).

C -! SUBCELIULAR LOCATION: Integral membrane protein.

C -! DOMAIN: The segment S4 is probably the voltage-sensor and is characterized by a series of positively charged amino acids at every third position.

C -! SIMILARITY: Belongs to the potassium channel family. H (Eag)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily.

-! SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

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                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Potassium voltage-gated channel subfamily H member 2 (Ether-a-go-go related gene potassium channel 1) (ERG1) (Ether-a-go-go related XCNH2 OR ERG.
                                                                                                                                                                                         ö
                                                                                                                                                  Length 5560;
                      protein;
                                                                                                                                                                                       0; Indela
PROSITE, PS50917; SPOC; 1.

Transcription regulation; Repressor; Developmental | Nuclear protein; Repeat; RNA-binding; Coiled coil; Alternative promoter usage; Alternative splicing. DOMAIN 554 632 RNA-BINDING (RRM) 1. DOMAIN 656 730 RNA-BINDING (RRM) 2. DOMAIN 734 806 RNA-BINDING (RRM) 3.
                                                                                                                                                    ; Score 29; DB 1; I
; Pred. No. 8.3e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ271210; CAB66135.1; -.
INTERPRO; IPR00595; CNMP_binding.
INTERPRO; IPR005967; ENG_CHANNEL.
INTERPRO; IPR005821; ION_LEANS.
INTERPRO; IPR001622; K+Channel_pore.
INTERPRO; IPR005820; M+Channel_nlg.
Pfam; PF00027; CNMP_binding; 1.
Pfam; PF00520; ion_trans; 1.
PRINTS; PR01470; ERGCHANNEL.
                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 6; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                     3430 SSGPSL 3435
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NCBI_TaxID=9031;
                                                                                                                                                                                                                                  SSGPSL
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MYCD MOUSE STANDARD; PRT; 935 AA.

G8VIM5; Q8C3W6; Q8VIL4;

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

10-OCT-2003 (Rel. 42, Last annotation update)

10-OCT-2003 (Rel. 42, Last annotation update)

MYCD OCT-2003 (Rel. 42, Last annotation update)

MYCD OR SRFC OF BSAC2.

MYCD OR SRFCP OR BSAC2.

BYCD OR SRFCP OR BSAC2.

MYCD OR SRFCP (Gradata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

MUSH TAXID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21332583; PubMed=11439182; Wang D.-Z., Chang P.S., Wang D.-Z., Chang P.S., Wang Z., Sutherland L., Richardson J.A., Small E., Krieg P.A., Olson E.N. Ball B., Krieg P.A., Olson E.N. and a myocardin, a transcriptional cofactor for serum response factor."; Cell 105:851-862(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, SUBCELLULAR LOCATION, INTERACTION WITH SRF, AND MUTAGENESIS OF 187-CLU--ARG-389 AND 408-ASP--LEU-410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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R SMART; SM00100; CNMP; 1.

R PROSITE; PS00889; CNMP BINDING_1; FALSE_NEG.

R PROSITE; PS00889; CNMP BINDING_2; FALSE_NEG.

R PROSITE; PS00889; CNMP BINDING_3; 1.

R PROSITE; PS00842; CNMP BINDING_3; 1.

Transport; Ion transport; Ionic channel; Voltage-gated channel;

M Glycoprotein; Multigene family.

T DOWN TER 1 103 CYTOPLASMIC (POTENTIAL).

T TRANSMEM 104 124 SEGMENT S1 (POTENTIAL).

T TRANSMEM 151 171 CYTOPLASMIC (POTENTIAL).

T TRANSMEM 193 213 SEGMENT S3 (POTENTIAL).

T TRANSMEM 193 213 SEGMENT S4 (POTENTIAL).

T TRANSMEM 193 214 SEGMENT S4 (POTENTIAL).

T TRANSMEM 193 214 SEGMENT S4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
SEGMENT S1 (POTENTIAL).
SEGMENT S2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
SEGMENT S5 (POTENTIAL).
SEGMENT S6 (POTENTIAL).
SEGMENT S6 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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SEQUENCE FROM N.A., AND REVISIONS OF 1-128.
MEDLINE=22317395; PubMed=12397177;
Wang D.-Z., Li S., Hockemeyer D., Sutherland L., Wang Z., Schratt Richardson J.A., Nordheim A., Olson E.N.;
Potentiation of serum response factor activity by a family of myocardin-related transcription factors.";
Proc. Natl. Acad. Sci. U.S.A. 99:14855-14860(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN=C57BL/6; TISSUE=Heart;
Sawada T., Okazaki T., Nakano H.;
"An alternative splicing form of myocardin (BSAC2), myocardin A
(BSAC2A).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
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Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  103 CYTOPLASMIC (POTENTIAL).
1124 SEGMENT S1 (POTENTIAL).
1711 SEGMENT S2 (POTENTIAL).
192 CYTOPLASMIC (POTENTIAL).
213 SEGMENT S4 (POTENTIAL).
254 SEGMENT S4 (POTENTIAL).
250 SEGMENT S4 (POTENTIAL).
251 SEGMENT S4 (POTENTIAL).
251 SEGMENT S6 (POTENTIAL).
366 SEGMENT S6 (POTENTIAL).
367 CYTOPLASMIC (POTENTIAL).
368 CYTOPLASMIC (POTENTIAL).
369 CYTOPLASMIC (POTENTIAL).
360 CYTOPLASMIC (POTENTIAL).
361 CYTOPLASMIC (POTENTIAL).
362 CNMP.
363 CYTOPLASMIC (POTENTIAL).
364 CYTOPLASMIC (POTENTIAL).
365 CNMP.
367 CYTOPLASMIC (POTENTIAL).
368 COTTOPLASMIC (POTENTIAL).
369 COTTOPLASMIC (POTENTIAL).
360 CYTOPLASMIC (POTENTIAL).
361 CYTOPLASMIC (POTENTIAL).
362 CNMP.
363 CYTOPLASMIC (POTENTIAL).
364 CYTOPLASMIC (POTENTIAL).
365 CNMP.
366 CYTOPLASMIC (POTENTIAL).
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526 AA;
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CARBOHYD
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us-09-848-834a-6.open.rsp
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RD MOI. Cell. BIOL. 23:4425-243/(2003).

RD SEQUENCE OF 728-935 FROM N.A.

SEGUENCE OF 728-935 FROM N.A.

SEGUENCE OF 728-935 FROM N.A.

REA SEGUENCE OF 728-935 FROM N.A.

RA SEGUENCE OF TISSUE-Embryonic heart;

RA MIXAIDO I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nadi K., Tomaru Y., Hasegawa T., Rachohach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Balke J.A., Eradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Balke J.A., Rawali T.A., Metuda H., Eatalov S., Beisel K.W.,

RA Anai A., Kawali T.A., Retcher C.F., Forreet A., Frezer K.S.,

R Ganterland T., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Anai A., Kawali H. W., Lee Y., Lenhard B., Lyons P.A.,

R Anai A., Kawali H., Marchiomi L., McKenzie L., Mixi H.,

RA Magashima T., Mumata K., Okido T., Peavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.L.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Partea G., Pesole G.,

RA Sundala R., Schneider C., Semple C.A., Setou M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Hirozane R., Washer L., Wahlestedt C., Wang Y., Warzanabe Y., Wall R.,

RA Hirozane R., Magner L., Wahlestedt C., Wang Y., Warzanabe Y., Wall R.,

RA Hirozane R., Magner L., Wahlestedt C., Wang Y., Warzanabe Y., Wall R.,

RA Hirozane R., Mayarshizaki Y., Saski K., Saski K., Sinkawa T., Rohen W., Saski K., Saski D., Shibate K., Lander E.S., Rogers J.,

RA Hara A., Hashizume W., Imotani K., Ishin Y., Ishinagwa R.,

Ranishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA "Mallagis of the mouse transcriptome based on functional annotation of K. (6), 770 full-length cobas." [4] SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL FUNCTION, TISSUE SPECIFICITY, AND INTERACTION WITH SRF. MEDLINE=22615366; PubMed=12663482; Memboff B.R., Hoofnagle M.H., Yoshida T., Sinha S., Dandre F., Wamhoff B.R., Hoofnagle M.H., Kremer B.E., Wang D.-Z., Olson B.N., Owens G.K., "Myocardin is a key regulator of CarG-dependent transcription of multiple smooth muscle marker genes."; Circ. Res. 92:854-864 (2003). Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

MEDINE=21403251; PubMed=11511353;

A Hauschka S.D.;
T cardiac Muscle.";

Myocardin. a novel potentiator of SRF-mediated transcription in cardiac muscle.";

Mol. Cell 8:1-2(2011)

L Mol. Cell 8:1-2(2011)

C multiple CArd boxes DNA sequence. Acts as a cofactor of serum response factor (SRF) with the potential to modulate SRF-target genes. Regulates the expression of a set of cardiac and smooth muscle-specific genes. Plays a crucial role in cardiogenesis and differentiation of the smooth muscle cell lineage (myogenesis).

May bind matrix attachment regions through its SAP domain.

-1- SUBUNIT: Homodimer (By similarity). Interacts with SRF, its association does not depend on specific DNA sequences for ternary

complex formation.
SUBGEL/ULAR LOCATION: Nuclear, with a punctate intranuclear pattern with exclusion from nuclei.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;

EMBL; AF384055; ARX1683.2; -.

BREL; AK984006; BAC3928.1; -.

BREL; AK984006; BAC3928.1; -.

BRI; PT0546; PT0698.

BRI; PT0717; PT0717.

MMI:217495; Strfp.

MGD; GO:0005534; C:nucleus, IDA.

GO; GO:0005534; C:nucleus, IDA.

GO; GO:0005534; E:protein binding; IPI.

GO; GO:0005534; E:protein binding; IPI.

GO; GO:0005534; P:protein binding; IPP.

GO; GO:0005644; P:protein binding; IPP.

GO; GO:0005644; P:protein binding; IPP.

GO; GO:0005664; P:regulation of external signals that reg. .; IDA.

GO; GO:0045661; P:regulation of myoblast differentiation; IMP.

INTERPRO; IRR00304; SAP.

FEam; PF02755; RREL; 1.

PEam; PF02755; RREL; 3.

SNART; SMOG13; SAP; 1.

BOR Transcription regulation; Activator; Nuclear protein; Coiled coil; This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). Missing (in isoform 2).
/FITG=VSP 007662.
Q -> QNSGAHEGHESSFSSPASSIHQPFSGTQADSSHSAG LNPCPKSFSIHPRKF (in isoform 2).
/FITG=VSP 007663.
ELR->PSF: ACTIVATION OF ANF PROMOTER ABOLISHED, NO BFPECT ON SN22 PROMOTER. DEL->PGH: ACTIVATION OF ANF PROMOTER. ABOLISHED, NO BFPECT ON SN22 PROMOTER. H -> N (IN REF. 4). RPEL 1.
RPEL 2.
RPEL 2.
GLN-RICH.
COILED COIL (POTENTIAL). COILED COIL (POTENTIAL). POLY-GLN. 11111111111111111111 Repeat; Alternative splicing.
REPEAT 62 87 RPE
REPEAT 106 131 RPE
DOMAIN 287 320 GLN
DOMAIN 380 414 SAF
DOWAIN 300 320 COI
DOWAIN 300 320 COI
DOWAIN 300 320 POL
VARSPLIC 1 128 Wis 389 410 81 408 387 81 CONFLICT MUTAGEN

Query Match
Best Local Similarity 83.3%; Pred, No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 110 110 E -> EA (IN REF. 4). 794 794 G -> D (IN REF. 3 AND 5). 935 AA; 101373 MW; C1D883EFBC181149 CRC64; CONFLICT CONFLICT SEQUENCE FT

1 SSGPSL 6 |||||: 906 SSGPSI 911

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0; Gaps

Search completed: March 10, 2004, 09:13:52 Job time : 3.09728 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2004, 08:58:54; Search time 1.8677 Seconds (without alignments) 309.015 Million cell updates/sec Run on:

US-09-848-834A-6 29 1 SSGPSL 6 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 segs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	nonstructural prot	transcription fact	hypothetical membr	polymerase-associa	uncharacterized co	hypothetical prote	clock	clock r	otein -		d	Ω H	н	hypothetical prote	inorganic diphosph	ORF Z protein - hu	cytochrome c [vali	conserved hypothet	hypothetical prote	hypothetical prote	,	histone HlA - Afri	1		conserved hypothet	ಹ	al	i D	딥
	д 	***	A53027	10	TH	^	S74453	T46659	844457	S30385	T04777	857150	T34060	T02850	T27121	C38230	C36817	CCEG	H83089	G75471	H72621	HSXL1A	151227	H287	B97655	714	7056	138	10	IO.
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hypothetical 36K g	hypothetical prote	adenylosuccinate s	3-isopropylmalate	AAA family ATPase	homeotic protein H	nitrogenase molybd	hypothetical prote	probable membrane	threonine synthase	hypothetical prote	probable transcrip	hypothetical prote	competence protein	probable membrane	amino acid transpo
JQ1660	AC2244	G69181	A26447	B90169	S71480	801839	H96536	T36256 ·	C75591	T52398	735666	875721	A12316	855124	B90504
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326	326	340	366	393	399	457	460	464	470	491	200	509	509	510	515
89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7	89.7		89.7	
56	56	26	56	56	56	56	56	26	56	56	26	56	26	56	56

ALIGNMENTS

		paramyxov.
		simian
		>
		protein
RESULT 1	JQ2040	nonstructural
E	g	ç

irus SV41

C;Species: simfan paramyxovirus SV41
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Jul-1999
C;Accession: JQ2040
B;Kawano, M.; Tsurudome, M.; Oki, N.; Nishio, M.; Komada, H.; Matsumura, H.; Kusagawa, J. Gen. Virol. 74, 911-916, 1993
A;Title: Sequence determination of the P gene of simian virus 41: presence of irregula A;Accession: JQ2040; MUID:93260408; PMID:8492098
A;Accession: JQ2040
A;Molecule type: genomic RNA
A;Residues: 1-225 <KAW>
A;Cross-references: GB:S60811; NID:9385516; PIDN:AAB26639.1; PID:g385517
C;Genetics:

C.Superfamily: simian paramyxovirus nonstructural protein V; V/P protein homology C;Keywords: alternative splicing; nonstructural protein F:1-163/Domain: V/P protein homology <VPN>

0; Gaps Query Match 100.0%; Score 29; DB 1; Length 225; Best Local Similarity 100.0%; Pred. No. 68; Matches 6; Conservative 0; Mismatches 0; Indels

144 SSGPSL 149 1 SEGPSL 6 à 셤

Transcription factor HES-1 - human
NyAlternate names: hairy protein homolog
()Species: Homo sapiens (man)
C)Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Dec-1999
C;Accession: A53027
E;Feder, J.N.; Li, L.; Jan, L.Y.; Jan, Y.N.
Genomics 20, 56-61, 1994
A;Title: Genomic cloning and chromosomal localization of HRY, the human homolog to the A;Title: Genomic as a second cloning and chromosomal localization of A;Title: Genomic A;Title: Genomic A;Accession: A53027; MUID:94292187; PMID:8020957
A;Accession: A53027
A;Accession: A53

100.0%; Score 29; DB 2; Length 280;

A;Map position: 3q28-3q29 C;Keywords: immediate-early protein

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A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Status: 1-589 <ARO-
A;Cross-references: EMBL:U17073; NID:9595951; PIDN:AAA57121.1; PID:9595952
A;Cross-references: Extain OR 74 A; isolate bdA; mycelia
R;McClung, C.R.; Fox, B.A.; Dunlap, J.C.
A;Title: The Neurospora clock gene frequency shares a sequence element with the Drosoph A;Reference number: S04653; MUID:89281721; PMID:2525233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nylrenate names: central clock component frq
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Date: 19-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 01-Dec-2000
C;Accession: T46659; S04653
R;Aronson, B.D.; Johnson, K.A.; Dunlap, J.C.
R;Aronson, B.D.; Johnson, K.A.; Dunlap, J.C.
A;Aronson, B.D.; Accession: Circadian clock locus frequency; protein encoded by a single open reading fram
A;Reference number: Z23120; MUID:94329580; PMID:8052643
A;Accession: T46659
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A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Molecule type: DNA
A;Rosidues: 1-532 (KAN>
A;Cross-references: EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA16605.1; PID:d10173
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cigoedies: Symethocytis sp.
A;Variety: PCC 6803
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: 874453
B;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. A;Kaneko, T.; Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA, Res. 3; 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                              Solvent-Producing Bacterium Cl
                          Q.; Gibson, R.;
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, .; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bact A;fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bact A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97171
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Reference number: Comparative Analysis of the Solvent-Producing Bact A;Reference number: Clostridium acetobutylicum AFCC824
C;Genetics: A;Genetics: A6600
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Matches 6; Conservative 0; Mismatches 0; Indels
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Matches 6; Conservative 0; Mismatches
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N,Alternate names: central clock component frg
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polymerate names: P protein
C:Species: simian paramyxovirus SV41
C:Species: simian paramyxovirus SV41
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C:Accession: 02041
R:Kawano, M.; Tsurudome, M.; Oki, N.; Nishio, M.; Komada, H.; Matsumura, H.; Kusagawa, S.; Cac. virol. 74, 911-916, 1993
A:Title: Sequence determination of the P gene of simian virus 41: presence of irregular A;Reference number: UQ2040; MUID:93260408; PMID:8492098
A;Accession: UQ2041
A;Accession: UQ2041
A;Accession: UQ2041
A;Accession: UQ2041
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S. Superfemily: simian paramyxovirus P protein; V/P protein homology C; Superfemily: simian paramyxovirus P protein; RNA editing P;1-163/Domain: V/P protein homology <VPN>
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100.0%; Score 29; DB 2;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                 Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches
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Best Local Similarity 100..
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T34660
R;Geisel, C.; Kramer, J.; Smith, A.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F28B3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZMSI protein - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein J2052; protein YJR127c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S57150; 843751
R;Rose, M; Koetter, P; Entian, K.D.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57132
A;Reference number: S57132
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A,Residues: 1-130 cROS>
A,Gross-references: EMBL:249627; NID:g1015856; PID:g1015857; MIPS:YJR127c
R,Thomas, D.; Barbey, R.; Surdin-Kerjan, Y
Exbmitted to the EMBL Data Library, December 1993
A,Reference number: 843751
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A,Introns: 253/3; 636/3; 1017/3
A,Note: P10M10.80
C,Superfamily: Arabidopsis thaliana hypothetical protein F10M10.80
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A;Residues: 'MHTN',18-1116,'IF',1119-1130,'H',1132-1142,'S' <THO>
A;Cross-references: EMBL:L26506; NID:g432497; PID:g432498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 29; DB 2; Length 1074; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels C
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A.Cross-references: SGD:S0003888; MIPS:YJR127c
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Best Local Similarity 100.8
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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C;Species: Homometers (man)
C;Species: Homometers (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: Sands
B;Accession: J; 290, 811-818, 1993
A;Title: The G99 gene in the human major histocompatibility complex encodes a novel prot A;Reference number: S30385
A;Accession: S30385
A;Accession: S30385
A;Accession: S30485
A;Accession: S30485
A;Accession: S30485
A;Accession: S30485
A;Cross-references: EMBL: X69838; NID:9287864, PIDN:CAA49491.1; PID:9287865
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology
P;641-673/Domain: ankyrin repeat homology <ANR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           period clock protein frq - Sordaria fimicola
C,Species: Sordaria fimicola
C,Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
C,Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Nov-1999
R,Merrow, M.W.; Dunlap, J.C.
BMBO J. 13, 2257-2266, 1994
A,Title: Intergeneric complementation of a circadian rhythmicity defect: phylogenetic cd
A,Reference number: 844457; MUID:94252311; PMID:8194516
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A,Residues: 1-997 <NMEN>
A,Residues: 1-997 <NMEN>
C,GOSS-references: EMBL:L14467; NID:g310366; PIDN:AAA20825.1; PID:g530050
C,GOST-INS:
A,GOST : frg
C,Keywords: circadian rhythm
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100.0%; Score 29; DB 2; Length 997;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                            Query Match
100.0%; Score 29; DB 2; Length 989;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels
A;Accession: S04653
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 'MGGN',206,'P',208-232,'H',234-989 <MCC>
A;Nete: the authors translated the initiation codon GTG as Val
C;Genetics:
A;Gene: frq
A;More: frq
A;More: VII R
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Matches 6; Conservative
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inorganic diphosphatase (EC 3.6.1.1) 1 - beet (fragments)
C;Species: Beta vulgaris (beet)
C;Date: 20-Aug-1999 #sequence revision 20-Aug-1999 #text_change 27-Oct-2003
C;Date: 20-Aug-1999 #sequence revision 20-Aug-1999 #text_change 27-Oct-2003
C;Accession: 238230; E38230; F38230
R;Sarafian, V.; Kim, Y.; Poole, R.J.; Rea, P.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1775-1779, 1992
A;Ritlen Molecular cloning and sequence of cDNA encoding the pyrophosphate-energized valuacement commber: A38230; MUD:92179265; PMID:1311852
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A,Residues: 29-52 <SAR3>
A,Residues: 29-52 <SAR3>
A,Bxperimental source: cultivar Detroit Dark
A,Note: sequence extracted from NOBI backbone (NCBIP:87195)
C,Superfamily: H(+)-translocating inorganic pyrophosphatase
C,Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: sequence extracted from NCBI backbone (NCBIP:87194)
A;Accession: F38230
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A;Residues: 1-16 <SAR1>
A;Note: sequence extracted from NCBI backbone (NCBIP:87192)
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Best Local Similarity 83.3%;
Matches 5; Conservative
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43 TSGPSL 48
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1 SSGPSL 6
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C. Species: Leishmania major
C. Date: 24-Mar-1999 #text_change 19-May-2000
C. Date: 24-Mar-1999 #tequence_revision 24-Mar-1999 #text_change 19-May-2000
C. Accession: F81462; T02850
C. Accession: F0.5 A. Jevos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A,Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-q A,Reference number: A81465; MUID:99178987; PMID:10077609
A,Accession: F81462
A,Accession: F81462
A,Status: preliminary
A,References: DNA
A,Residues: 1-1487
A,Residues: 1-1487
A,Residues: L-1487
A,Residues: Residues: R
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A; Reference number: 220314
A; Reference number: 220314
A; Reference number: 220314
A; Reseasion: T27121
A; Molecule type: DNA
A; Residues: 1-1564 <WIL>
A; Cosperimental source: clone Y53C10A
A; Cosperimental source: clone Y53C10A
A; Genetics:
C; Genetics:
C; Genetics:
C; Genetics: 43/3; 92/2; 148/2; 226/3; 354/1; 712/3; 817/1; 875/1; 916/3; 984/3; 1069/2;
C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
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                                            A.Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rosidues: 1-22-3 CGEP.
A,Rosidues: 1-22-3 CGEP.
A,Gross-references: EMBLAF003136; PIDN:AAB93634.1; GSPDB:GN00019; CESP:F28B3.2
A,Roserimental source: strain Bristol N2; clone F28B3
C,Genetics:
A,Moene: CESP:F28B3.2
A,Map position: 1
C;Superfamily: Caenorhabditis elegans hypothetical protein F28B3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aypothetical protein L1439.2 [imported] - Leishmania major (strain Friedlin)
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93.1%; Score 27; DB 2; Length 1564;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels
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93.1%; Score 27; DB 2; Length 1487;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels
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93.1%; Score 27; DB 2; Length 222;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels
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Sequence 224, App
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Sequence 7, Appli
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Sequence 209, App
Sequence 209, App
Sequence 49, Appl
Sequence 224, App
Sequence 224, App
Sequence 224, App
Sequence 224, App
Sequence 349, Appl
                                                                                                                             March 10, 2004, 09:16:59 ; Search time 3.14397 Seconds (without alignments) 268.645 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/PCT_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_PUBCOMB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/PCT_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USOG_NEW_PUB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USOG_PUBCOMB.pep:*

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GenCore version 5.1.6
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4 US-10-285-976-224

US-09-848-834A-7

US-09-848-834A-7

US-10-223-711-4

US-10-223-711-4

US-10-371-069-209

US-10-371-069-209

US-10-371-260-209

US-10-371-260-209

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US-10-371-260-209

US-10-371-260-209

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Maximum Match 100%
Listing first 45 summaries
                                                                                      - protein search, using sw model
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Maximum DB seq length: 200000000
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ALIGNMENTS

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RESULT 1
US-09-848-834A-5
i Sequence 5, Application US/09848834A
i Patent No. US20020076416A1
i GENERAL INFORMATION:
i APPLICANT: Aphton Corporation
i TITLE OF INVENTION: Chimeric Peptide Immunogens
i TITLE OF INVENTION: Chimeric Peptide Immunogens
i FILE REFERENCE: 1102865-004
i CURRENT APPLICATION NUMBER: US/09/848,834A
i CURRENT PILING DATE: 2001-05-04
i PRIOR APPLICATION NUMBER: 60/202,328
i PRIOR PILING DATE: 2000-05-05
i RIGHT FILE OF SEQ ID NOS: 20
i SEQ ID NOS: 20
i SEQ ID NO 5
i LENGTH: A
i TYPE: PRT
i OTHER INFORMATION: Synthetic peptide
i FBATURE:
i OTHER INFORMATION: Synthetic peptide
i FBATURE:
i OTHER INFORMATION: Synthetic peptide
i GPSANIS
i GPSANIS
i GPSANIS
i GPSL 4
i GPSL 5
i BAPLICANT: Rhee, Chae-Seo
i APPLICANT: Rhee, Chae-Seo
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FEATURE:
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APPLICANT: Wu, Christina

APPLICANT: Leoni, Lorenzo M.

APPLICANT: Corr, Maripat

APPLICANT: Corr, Maripat

APPLICANT: Carson, Dennis A.

APPLICANT: Carson, Dennis A.

APPLICANT: Trace of the University of California

TITLE OF INVENTION: Wht and Frizzled Receptors as Targets for Immunotherapy,

TITLE OF INVENTION: MH and Frizzled Receptors as Targets for Immunotherapy,

TITLE OF INVENTION: WHORE: US/10/285,976

CURRENT FILING DATE: 2002-11-01

PRIOR PAPLICATION NUMBER: US 60/281,995

PRIOR PAPLICATION NUMBER: WO PCT/US02/13802

PRIOR APPLICATION NUMBER: WO PCT/US02/13802

PRIOR STING DATE: 2001-05-01

PRIOR APPLICATION NUMBER: WO PCT/US02/13802

SOFTWARE: Patentin Ver: 2.1
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OTHER INFORMATION: Sequence
US-10-285-976-224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels
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Publication No. US20030113344A1
GENERAL INFORMATION:
APPLICANT: Bakaletz, Lauren O.
APPLICANT: Raumaya, Pravin T.P.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-848-834A-6; Sequence 6, Application US/09848834A Patent No. US20020076416A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-223-711-4
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100.0%; Score 21; DB 9; L
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 4; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3:0
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GENERAL INFORMATION:
APPLICANT: Braun, Ralph P.
APPLICANT: Thomsen, Lindy
APPLICANT: Wan-Wely, Catherine
TITLE OF INVENTION: Adjuvant
FILE REFERENCE: 031267-015
CURRENT APPLICATION NUMBER: US/10/102,622
CURRENT FILING DATE: 2002-03-19
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FABLEEQ for Windows Version 4.0
FILE REFERENCE: 16525/04058
CURRENT APPLICATION NUMBER: US/10/223,711
CURRENT FILING DATE: 2002-08-19
FRIOR APPLICATION NUMBER: 09/148,711
FRIOR FILING DATE: 1990-09-04
FRIOR FILING DATE: 1990-06-02
FRIOR FILING DATE: 1990-06-02
NUMBER: OF SEQ ID NOS: 12
SOFTWARE: PALENTIN VERSION 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic construct US-10-223-711-4
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). Patent No. US20020076416A1
; GENERAL INFORMATION:
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US-10-102-622-2
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us-09-848-834a-5.open.rapb

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Query Match
100.0%; Score 21; DB 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 21; DB 15; Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: HBV 360 (peptide 1039.01) US-10-371-260-209
                                                                                                                                                                                                                                                                                                                                    FEATURE:
; OTHER INFORMATION: HBV 360 (peptide 1039.01)
US-10-371-645-209
        PRIOR APPLICATION NUMBER: US 09/078, 904
PRIOR APPLICATION NUMBER: US 09/078, 904
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 10
CURRENT APPLICATION NUMBER: US/10/371,645 CURRENT FILING DATE: 2003-06-20
                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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PUBLICATION NO. US20030216342A1
FURDICATION NO. US20030216342A1
GREEKLI INFORMATION:
APPLICANT: EPINMUNE Inc.
APPLICANT: Hermanson, Gary G.
APPLICANT: Hermanson, Gary G.
APPLICANT: Ishioka, dienn Y.
APPLICANT: Livingston, Brian
APPLICANT: Specification NUMBER: US/10/371,069
CURRENT APPLICATION NUMBER: US 09/078,904
FRICK APPLICATION NUMBER: US 09/078,904
FRICK APPLICANTON NUMBER: US 09/078,904
FRICK APPLICANTON NUMBER: US 09/078,904
FRICK APPLICANTON NUMBER: US 09/078,751
FRICK FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SED ID NO 2094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
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100.0%; Score 21; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                           100.0%; Score 21; DB 14;
100.0%; Pred. No. 7.1e+05;
7ative 0; Mismatches 0;
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US-10-371-069-209
                                ; TYPE: PRT
; ORGANISM: Artificial Sequence
; PEATURE:
OTHER INFORMATION: HSV CD8 in BALB/C mice
US-10-102-622-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 209, Application US/10371645
Publication No. US20030216343A1
GENERAL INFORMATION:
APPLICANT: BPIMMUNE Inc.
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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LENGTH: 10
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Sequence 49, Application US/10373238
Publication No. US20040014083A1
GENERAL INFORMATION
APPLICANT: General Atomics
TITLE OF INVENTION: DETECTION OF HETERODUPLEX POLYNUCLEOTIDES USING MUTANT
                                                                                                                                                                                                                                                                                   Sequence 209, Application US/10371260
Sequence 209, Application US/10371260
Sublication No. US2003022028541
Sublication No. US2003022028541
Sublication No. US2003022028541
APPLICANT: Fikes, John D.
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro.
APPLICANT: Sette, Alessandro.
APPLICANT: Chemut, Robert W.
APPLICANT: Chemut, Robert W.
APPLICANT: Epimunu Inc.
APPLICANT: Epimunu Fixes
Supression Vectors for Stimulating an TITLE OF INVENTION: Expression Vectors for Stimulating an FILIE REFERENCE: 39964-20022.13
CURRENT FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 209
LENGTH: 10
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Length 10;
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APPLICANT: Fixes, John D.
APPLICANT: Fixes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Hermanson, Gary G.
APPLICANT: Hermanson, Glenn Y.
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Livingston, Brian
APPLICANT: Epimume Inc.
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-2002.1.
CURRENT APPLICATION NUMBER: US/10/371,645
CURRENT FILING DATE: 2003-06-20
FRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-14
FRIOR FILING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: HBV env 359 (peptide 1039.06)
           Application US/10371645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
           Sequence 224, Application US/10:
Publication No. US20030216343A1
GENERAL INFORMATION:
APPLICANT: EPIMUNE Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GPSL 4
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Matches
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TITLE OF INVENTION: NUCLBIC ACID REPAIR ENZYMES WITH ATTENUATED CATALYTIC ACTIVITY FILE REFERENCE: 46699-20004.20
CURRENT PEDICATION NUMBER: US/10/373,238
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: 09/514,016
PRIOR APPLICATION NUMBER: 09/514,016
PRIOR PELING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 84
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 49
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Pb (III) ion OTHER INFORMATION: binding protein sequence.
PUBLICATION INFORMATION:
PATENT DOCUMENT NUMBER: S,679,548
PATENT FILMO DATE: 1993-06-14
PUBLICATION DATE: 1997-10-21
US-10-373-238-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 21; DB 15; Length 10; Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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. OTHER INFORMATION: HBV env 359 (peptide 1039.06)
US-10-31-069-224
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Best Local Similarity
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US-10-371-069-224
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Sequence 224, Application US/10371260

Sequence 224, Application US/10371260

Publication No. US20030220285A1

GENERAL INFORMATION:

APPLICANT: BINMUNE Inc.

APPLICANT: Bites, John D.

APPLICANT: Bites, John D.

APPLICANT: Islieva, John D.

APPLICANT: Islieva, John D.

APPLICANT: Islieva, John D.

APPLICANT: Livingston, Brian

APPLICANT: Livingston, Immune Response and Methods of Using the Same

TILLE OF INVENTION: Expression Vectors for Stimulating an

TILLE OF INVENTION: Expression Vectors for Stimulating an

TILLE OF INVENTION: By 1000-1.3

CURRENT APPLICATION NUMBER: US/10/371,260

CURRENT APPLICATION NUMBER: US 09/078,904

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

PRIOR FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 463

LENGTH: LAND APPLICATION NUMBER: US 08/085,751

PRIOR FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 463

LENGTH: LAND APPLICATION NUMBER: US 08/085,751

PRIOR FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 463

LENGTH: LAND APPLICATION NUMBER: US 08/085,751

PRIOR FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 463

LENGTH: LAND APPLICATION NUMBER: US 08/085,751

PRIOR FILING DATE: 1998-05-13

NUMBER OF SEQ ID NOS: 463

LENGTH: LAND APPLICATION NUMBER: US 08/085,751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: HBV env 359 (peptide 1039.06)
US-10-371-260-224
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Best Local Similarity
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RESULT 12 US-10-371-645-224

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Gaps
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                                                                                                                                                                                                                                                            APPLICANT: Achle, Wolfgang
APPLICANT: Baldwin, Toby L.
APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Warray, Christopher J.
APPLICANT: Warnay, Huaming
APPLICANT: Warney, Huaming
APPLICANT: Warney, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
FILE REPERENCE: GG600
CURRENT APPLICATION NUMBER: US/09/954,385
CURRENT FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 433
SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 21; DB 14; Length 14; Best Local Similarity 100.0%; Pred. No. 5e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 4.38+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Sequence 10. Application US/10024123
Publication No-US20030022263A1
Sequence 10. Application US/2003002263A1
Septicant: Kaetan, Michael
APPLICANT: Kaetan, Michael
APPLICANT: Kim, Seong-Tae
APPLICANT: Kim, Dae-Sik
APPLICANT: Lim, Dae-Sik
TITLE OF INVENTION: ATM Kinase Modulation for Screening and
TITLE OF INVENTION: ATM Finase Modulation for Screening and
TITLE OF INVENTION: ATM Finase Modulation for Screening and
TITLE OF INVENTION: ATM Finase Modulation for Screening and
0; Indels
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CURRENT FILIDRO DATE: 2001-12-17
CURRENT FILING DATE: 1099-09-21
PRIOR PAPLICATION NUMBER: 09/400,653
PRIOR FILING DATE: 1999-02-10
PRIOR PILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
TENDETH: 14
0; Mismatches
                                                                                                                                                                                              Sequence 349, Application US/09954385 Publication No. US20030100467A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; CIHER INFORMATION: binding peptide US-09-954-385-349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
    4; Conservative
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US-10-024-123-10
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                                                                              7 GPSL 10
                                        1 GPSL 4
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US-09-954-385-349
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LENGTH: 12
    Matches
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Search completed: March 10, 2004, 10:25:47 Job time: 3.14397 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

March 10, 2004, 08:58:53; Search time 0.731517 Seconds (without alignments) 284.724 Million cell updates/sec Run on:

US-09-848-834A-5 21 1 GPSL 4

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		diploptera	locusta mig	net	artemia sal	Ω	bos taurus	homo sapien	mus musculu	rhodospiril	homo sapien	mycobacteri	rhodospiril	rhodospiril	rhodospiril	euglena gra	synechocyst	rhodopila g	rhodopseudo	ascaris suu	rhizobium l	mns mnscnln	homo sapien	synechococc	bacillus su	synechocyst	xanthomonas	sus scrofa	homo sapien	sus scrofa	mus musculu	agrobacteri	mycobacteri	DON'T CHICA
	escri	P82373	346	4153	1904	5041	Q02371	095167	•		002325	P46389	P00088	P00086	P00087	P00076	P42351	P00080	P00084	P92505	P23716	P01823	P56279	024694	P24469	P73315	QBppc2	019175	P01178	P01177	Q9da01	_	Q9kh57	017070
		DIUH DIPPU	DIUH_LOCMI	DIUH PERAM	NUSM_ARTSA	MAUD METFL	NI 9M BOVIN	NI 9M HUMAN		CY22_RHOFU	PRGB HUMAN	RS6 MYCLE	CY22 RHOMO	CY21 RHOFU	CY21 RHOMO	CYC EUGGR	CSSL SYNY3	CY2 RHOGL	CY2_RHOAC	CYCZ ASCSU	NOLE RHILP	HV47 MOUSE	TCLA HUMAN	RL22_SYNP6	C5S0_BACSU	RL22_SYNY3	Y764 XANAC	KC1A_PIG	NEU1 HUMAN	NEU1 PIG				THE STATE OF THE PARTY OF THE P
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ALIGNMENTS

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46 AA,	update)	annotation update)	cockroach). poda; Insecta; Pto	Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Bla Blaberidae, Diploptera.		METRY.		, Zhang J., Tobe	terization of a		Froc. Natl. Acad. Sci. U.S.A. 97:0469-6474(2000). -1- FUNCTION: Regulation of fluid secretion. Stimulates primary	secretion by Malpighian tubules and causes a dose-dependent etimulation of camp layels in the fumiles. Has a greater of	ions. In vitro,	iller diuretic ho		MASS SPECTROMETRY: MW=5322; MW_ERR=0.1; METHOD=Electrospray	sauvagine/ cor cicocropin-reseasing					200	693CD9A16E47F67E CRC64;	21; DB 1; Le No. 1.3e+02; atches 0;			-	46 AB.	
PRT;	L)	st annotatic (Diuretic r	itic beetle ropoda; Hexa	, Dictyopter		MASS SPECTRO	a cardiaca; =10841553;	Schegg K.M.,	ones: charac		of fluid se	ian tubules layala in th	+) then K(+)	effects with the smaller	: Secreted.	W=5322; MW_E	n -	corticoliberin.	rtc_normn.	hormn; 1.		NO FER COLUMN	•	100.0%; Score 100.0%; Pred. ive 0; Mism				PRT;	Created)
STANDARD;	40,	(Rel. 43, Last mone class I (inctata (Pac etazoa; Arth	thopteroidea Diploptera.	984;	NCTION, AND	, and Corpor, 0924; PubMed	ilchak R.J.,	schooley D.A.; "Cockroach diuretic hormones: characterization	nsects.";	Acad. Sci. U : Regulation	n by Malpigh	sport of Na (synergistic effects	LAR LOCATION	CTROMETRY: M	Simirakiii: Belongs to th factor/urotensin I family	IPR000187, corticoliberi	8003621; Diu 3; CRF; 1.	4750, Diurto	100039; CRF; 1. PS00511; CRF; 1	Amidation.	9	100 Similarity 100 4; Conservative	4.		_	STANDARD;	(Rel. 20, Cr
DIPPU DIUM DIPPU	2001	15-MAR-2004 (Rel. 43, Last annotation update Diuretic hormone class I (Diuretic peptide)	Diploptera punctata (Pacific beetle Eukaryota; Metazoa; Arthropoda; Hexa	Neoptera; Or Blaberidae;	NCBI_TaxID=6984;	SEQUENCE, FU	TISSUE=Brain, and Corpora cardiaca; MEDLINE=20300924; PubMed=10841553;	Furuya K., Milchak R.J.,	Schooley D.A "Cockroach d	peptide in i	-I - FUNCTION	Becretio	the tran	synergistic			factor		Incerpro; 1F Pfam; PF0047	•••	SMART; SM00039; PROSITE; PS00511		SEQUENCE 4	Query Match Best Local Simi Matches 4;	1 GPSL	3-6	13045 4.	LT 2 LOCMI DIUH LOCKI	P23465; 01-NOV-1991
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MOD RES 46
SEQUENCE 46 AA; 5
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P19047;
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NUSM_ARTSA
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE=93174045; PubMed=1337794;
MEDLINE=93174045; PubMed=1337794;
May I., Patel M., Coast G.M., Totty N.F., Mallet A.I.,
Goldsworthy G.J.;
"Isolation, characterization and biological activity of a CRF-related
diuretic peptide from Periplaneta americana L.";
Regul. Pept. 42:111-122(1992).
Regul. Pept. 42:111-122(1992).
Regul. Pept. 82:111-122(1992).
Secretion by Malpighian tubules and causes a dose-dependent
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01-NOV-1991 (Rel. 20, Last sequence update)
15-MRA-2004 (Rel. 43, Last annotation update)
Diuretic hormone (DH) (Diuretic peptide) (DP).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Prerygota;
Rooptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                          MEDLINE=91378968; PubMed=1654896; Lehmberg E., Ota R.B., Furuya K., King D.S., Applebaum S.W., Ferenz H.-D., Schooly D.A.; "Identification of a diuretic hormone of Locusta migratoria."; Biochem. Biophys. Res. Commun. 179:1036-1041(1991).
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P41538,
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Diuretic hormone (DH) (Diuretic peptide) (DP).
Periplaneta americana (American cockroach).
Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; NCL TaxID=6978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 21; DB 1; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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SEQUENCE 46 AA; 5364 MW; E063260E74939763 CRC64;
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TISSUE=Brain;
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Mikazyota, Metazoa, Arthropoda, Crustacea, Branchiopoda, Anostraca,
Artemidae, Artemia.
WCBI_TaxID=85549;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=88289417; PubMed=3135541;
Batuecas B., Garesse R., Calleja M., Valverde J.R., Marco R.;
"Genome organization of Artemia mitochondrial DNA.";
Nucleic Acids Res. 16:6515-6529(1988).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 28, Last annotation update)
NADH-ubiquinone oxidoreductase chain 5 (EC 1.6.5.3) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 100.0%; Score 21; DB 1; Length 59; Local Similarity 100.0%; Pred. No. 1.7e+02; Pred. 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   Length 46;
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100.0%; Score 21; DB 1; Length 46
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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6938D47CB5AF2BA5 CRC64;
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Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
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MAUD METFL
TD WAUD METFL STANDARD;
AC C56416; Q56424; Q9RAN3;
DT 01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Artemia salina (Brine shrimp).
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46 AA; 5285 MW;
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sequencing proteins using the polymerase chain reaction.";
J. Mol. Biol. 226:1051-1072(1992).
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37
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                                        ACETYLATION
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095167;
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01-UUL-1993 (Rel. 26, Last sequence update)
10-UUL-1993 (Rel. 42, Last annotation update)
NADH-ubiquinone oxidoreductase B9 subunit (EC 1.6.5.3) (EC 1.6.99.3)
(Complex 1-89) (C1-89).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
[1]
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MEDLINE=92389317; PubMed=1518044;
MAlker J.E., Arizmendi J.M., Dupuis A., Fearnley I.M., Finel M.,
Malker, Pilkington S.J., Runswick M.J., Skehel J.M.;
Medd S.M., Pilkington S.J., Runswick M.J., Skehel J.M.;
"Sequences of 20 subunits of NADH:ubiquinone oxidoreductase from
bovine heart mitochondria. Application of a novel strategy for
                                            Methylobacillus flagellatum.
Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales,
Methylophilaceae, Methylobacillus.
NCBI_TaxID=405;
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STRAIN=KT / ATTC 51484 / DSM 6875 / VKM B-1610;
STRAINS X. ATTC 51484 / DSM 6875 / VKM B-1610;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY BE SPECIFICALLY INVOLVED IN THE PROCESSING,
TRANSPORT, AND/OR MAYINAATION OF THE MADH BETA-SUBUNIT.
                                                                                                                                                  Gak E.R., Chistoserdov A.Y., Lidstrom M.E.;
Cloning, sequencing, and mutation of a gene for azurin in
Methylobacillus flagellatum KT.";
J. Bacteriol. 177:4575-4578(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 1; Length 79; 100.0%; Pred. No. 2.2e+02; tive 0; Mismatches 0; Indels
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50 51 34 8517 NW; B4536D2B4A312CEF CRC64;
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Methylamine utilization protein maub (Fragments).
                                                                                                            SEQUENCE FROM N.A.
STRAIN-KT / ATTC 51484 / DSM 6875 / VKM B-1610;
MEDLINE-95362696; PubMed=7635847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 AA
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Best Local Similarity
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Q02371;
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MEDLINE=55046811; PubMed=7958365; PearThey LW., Skehell J.M., Walker J.E.; PearThey LW., Skehell J.M., Walker J.E.; PearThey LW., Skehell J.M., Walker J.E.; Electropray ionization mass spectrometric analysis of subunits of NADH:ubiquinone oxidoreductase (complex I) from bovine heart mitochondria.; Plans. 22:551-555(1994).

-I- FUNCTION: Transfer of electrons from NADH to the respiratory on Anion. The immediate electron acceptor for the enzyme is believed to be ubiquinone.

-I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

-I- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + reduced acceptor.

-I- SUBGENLIAR LOCATION: Integral membrane protein. Mitochondrial
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15-UTL-1999 (Rel. 38, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
MADH-ubiquinone oxidoreductase B9 subunit (EC 1.6.5.3) (EC 1.6.99.3)
(Complex I-B9) (CI-B9)
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MEDLINE=20499367; PubMed=11042152;
Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
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BUBLINES-89997250. PubMed=9878551;

LOEffen J.D.C.W., Triepels R.H., van den Heuvel L., Schuelke M.,

Buskens C.A.F., Smeets R.J.F., Trijbels J.M.F., Smeitink J.A.M.;

Enona de eight nuclear encoded subunits of NAPH-ubiquinone
oxidoreductase; human complex I cDNA characterization completed.";

Biochem. Biophys. Res. Commun. 253:415-422(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S28248; S28248.
Oxidoreductase; Ubiquinone; NAD; Mitochondrion; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE COMPLEX I B9 SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 1; Length 83; 100.0%; Pred. No. 2.3e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1B7B031860DB9370 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 AA; 9218 MW;
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TO THE STATE STATE
Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W., Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.; "Cloning and functional analysis of cDNAs with open reading frames for 300 previously undefined genes expressed in CD34+ hematopoietic stem/brogenitor cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to be ubiquinone.
--- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
--- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
---- SUBDUXIT: Mammalian complex I is composed of 45 different subunits.
---- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 603832; -. GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; TAS. Oxidoreductase; Ubiquinone; NAD; Mirochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE COMPLEX I B9 SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 21; DB 1; Length 84; 100.0%; Pred. No. 2.3e+02; Ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 AA; 9279 MW; 38B27A96D7A05D31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF044955; AAD05420.1; -.
EMBL; AF070653; AAD20959.1; -.
EMBL; BC022369; AAH22369.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, JE0379; JE0379.
Genew; HGNC:7686; NDUFA3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inner membrane
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GPSL 4
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Conservative
                                                                                                                  STANDARD;
         Local Similarity es 4; Conserv
                                                            75 GPSL 78
                                          1 GPSL 4
                                                                                                                                      21-JUL-1986
21-JUL-1986
                                                                                                                 CY22 RHOFU
P00089;
Query Match
                                                                                                     CY22 RHOFU
ID CY22 RH
AC P00089;
DT 21-JUL-
DT 21-JUL-
                                ö
                                                                                                                              84 AA.
                                                                                                                                     09C091;
28-FBB-2003 (Rel. 41, Created)
                                                                       75 GPSL 78
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NI9M_MOUSE ID _NI9M_MOUSE

RESULT 8

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                                                                                                                                                                                                                                                 TRAINE-STBL/GG; TISSUE-Heart, and Tongue;

KRAWAI CTSTBL/GG; TISSUE-Heart, and Tongue;

KRAWAI CTSTBL/GG; TISSUE-Heart, and Tongue;

KRAWAI CTSTBL/GG; TISSUE-Heart, and Tongue;

KRAWAI CTSTAINE-STOREST;

KRAWAI CT, SAIDARDA K., SHIBMID K., KONDO H., Adachi J., Flukuda S.,

AZARAWA T., HATA A., FIRMINIAN Y., KONDO B., Yamanaka I.,

SAICO T., OKAZAKI Y., GOJODOTI T., BONDO H., KABUKAWA T., SAILO R.,

KAGCER K., MARGHOAT T., ASHDUNTAR M., BARAION B., KOCHIWA H.,

KAGCER K., MARGHOAT T., KINARIGO I., PEGOLE G., QUACKENDUSH J.,

KAGLI I. M., STAUNII F., SIZUKI R., TOMITA M., WAGHAR L., WARDIO T.,

SARAI K., OKIGO T., FULUND M., AONO H., BALGATCHII R., BARSHO T.,

SARAI K., DOFFELLI D., BOJUNGA N., CARNICA M., CARIBOLAI M.,

ROWATGHOELIM M., TELECAPER C., FULUL A., KAMIYA M., LOE N.H.

LYONS P., MARCHIONNI L., MASHIMA J., MAZZARCHII J., MOMDAGETTS P.,

LYONS P., MARCHIONNI L., MASHIMA J., MAZZARCHII J., MOMDAGETTS P.,

RA GASAKI H., SALO K., SCHOCHDACH C., SEVA T., Shibata Y., Storich K.-F.,

SA SARAI H., TOYO-OKA K., WANG K.H., WANTELAKER C., WILMING I.,

RA WYNERAWA BOYIS R., YOSHIGA K., HABSEGBAWA Y., KAWAJI H., KOHLEUKI S.,

RA HAVARAWA BOYIS R., YOSHIGA K., HABSEGBAWA Y., KAWAJI H., KOHLEUKI S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).

-!- FUNCTION: Transfer of electrons from NADH to the respiratory chain. The immediate electron acceptor for the enzyme is believed to be ubiquinone (By similarity).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-!- SUBGUNIT: Mammalian complex I is composed of 45 different subunits.
-!- SUBGELIULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
28-FEB-2003 (Rel. 41, Last sequence update)
LoCTr-2003 (Rel. 42, Last annotation update)
NADH-ubiquinone oxidoreductase B9 subunit (EC 1.6.5.3) (EC 1.6.99.3)
(Complex I-B9) (CI-B9).
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AK019099; BAB31545.1; -.
EMBL; AK003133; BAB22593.1; -.
MGD; MGI:1913341; Ndufa3.
Oxidoreducrese; Ubiquinone; NAD; Mitochondrion; Transmembrane.
TRANSMEM 19 39
SEQUENCE 84 AA; 9331 MW; B05E59B217D95A92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inner membrane (By similarity).
-!- SIMILARITY: BELONGS TO THE COMPLEX I B9 SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 84;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 01, Created)
(Rel. 01, Last sequence update)
                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                             NCBI TaxID=10090;
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us-09-848-834a-5.open.rsp

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GPSL 33
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SIGNAL
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RS6_MYCLE
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DR HSSP; P00004; 1WEJ.

DR HSSP; P00004; 1WEJ.

DR InterPro; 1PR000345; Cyt_CTAB.

DR InterPro; 1PR000345; Cyt_CTAB.

DR PRINTS; PR000044; CYTCHRWECIAB.

DR PRINTS; PR000045; CYTCHRWECIAB.

DR PROSITE; PR00190; CYTCHRWECIAB.

FT BINDING 13 13 HEWE (COVALENT).

FT BINDING 13 13 HEWE (COVALENT).

FT BINDING 14 IN BOLECULES).

CO CALENT).

FT RON (HEWE AXIAL LIGAND).

CO CALENT).

TE TO NW; ESI762ABACBD42D CRC64;

CO CALENTS.

CO CALENTS.

TO NW; ESI762ABACBD42D CRC64;

CO CALENTS.

TO NW; ESI762ABACBD42D CRC64;

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TO NW; ESI762ABACBD42D CRC64;

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CO CALEN
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                                                                                                                                                                                                                                                                                       "Cytochrome of sequence variation among the recognised species of purple nonsulphur photosynthetic bacteria.";
Nature 278:659-660 (1979).
-!- FUNCTION: CYTOCHROME OI IS FOUND MAINLY IN PURPLE, NONSULFUR, PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOSHOSPHORYLATION PATHWAY. HOMEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA.

PIR; A00081; CCOFF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Multiple members of the plasminogen-apolipoprotein(a) gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Phaeospirillum.
                                                                                                                                                                                                              MEDLINE=79199667, PubMed=221822;
Ambler R.P., Daniel M., Hermoso J., Meyer T.E., Bartsch R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=2235990; Pubmed=1379800;
Medisabach L., Treadwell B.V.;
"A plasminogen-related gene is expressed in cancer cells.";
Biochem. Biophys. Res. Commun. 186:1108-1114(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
     01-NOV-1988 (Rel. 09, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasminogen-related protein B precursor.
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MEDLINE=92207924; PubMed=1554698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochemistry 31:3113-3118 (1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                          Cytochrome C2, iso-2.
Rhodospirillum fulvum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPSL 4
                                                                                                                                           NCBI_TaxID=1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLGL OR PRGB.
Homo sapiens
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                                                                                                                                                                                                                                                                           Kamen M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRGB HUMAN
                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRGB_HUMAN
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     à
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MEDLINE=22388257, PubMed=12477932,
A Grausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A strausberg R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Uddin T.B., Toshiyuki S., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Uddin T.B., Toshiyuki S., Carninoi P., Prange C.,
A Rha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
BOSAK S.A., McKwarna F.J., McKernan K.J., Malek J.A., Gunzratne P.H.,
R.A Richards S., Worley K.C., Holton E., Retterman M., Madan A., Gay L.J., Hulyk S.W.,
R.A Hidland D.K., Muzzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R.A Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Paleksley R.W., Maryinski M.I., Skalska U., Smailus D.E.,
R.A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
A Conson and mouse cDNA sequences.,
Brown at Silve Brown and may result in the localization of activity to pleaminogen and may result in the localization of activity to at sites necessary for extracellular matrix destruction.

-1 - SUMILARITY: Contains 1 PAN domin.
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BY SIMILARITY.
BY SIMILARITY.
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20 96 P
49 73 B
53 61 B
96 AA; 10971 MW;
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InterPro; IPR003609; Pan_app.
Pfam; PF00024; PAN; 1.
SMART; SM00473; PAN_AP; 1.
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96
73
61
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Ambler R.P.;
Submitted (JUN-1977) to the PIR data bank.
-!-FUNCTION: CYTOCHROME CZ IS FOUND MAINLY IN PURPLE, NONSULFUR,
-!-FUNCTION: GACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR
TO THE OXIDIZED BACTERIOCHLOROPHYLL, IN THE PHOTOPHOSPHORYLAITON
PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN
AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA.
                                                                                                                                                                                                            (In) Matsubara H., Yamanaka T. (eds.);
Evolution of protein molecules, pp.311-322, Japan Scientific Societies
Press/Center for Academic Publications, Tokyo (1978).
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Evolution of protein molecules, pp.311-322, Japan Scientific Societies
Press/Center for Academic Publications, Tokyo (1978).
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-!- FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR, PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria, Proteobacteria, Alphaproteobacteria, Rhodospirillales,
Rhodospirillaceae; Phaeospirillum.
NCBI_TaxID=1082;
Cytochrome C2, iso-2.
Rhodospirillum molischianum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Phaeospirillum.
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13 13 HEME (COVALENT).
14 I FON (HEME AXIAL LIGAND).
75 75 IRON (HEME AXIAL LIGAND).
97 AA, 10222 MW; 5AICBC489BODBFB6 CRC64;
                                                                                                                                                 Ambler R.P., Meyer T.E., Bartsch R.G., Kamen M.D.,
Unpublished results, cited by:
Ambler R.P.,
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Unpublished results, cited by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 1; I
Pred. No. 2.7e+02;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, P00004, 1WEJ.
InterPro; IPR003088; Cyt_CI.
InterPro; IPR003245; Cyt_CIAB.
InterPro; IPR000345; Cyt_CIAB.
FRIMT, PF000345; Cyt_CIAB.
FRINTS; PR00064; CYTCHRNEGIAB.
PRODOM; P0000375; Cyt_CIAB. 1.
PROSITE; PS00190; CYTCHRNEGIAB.
BLOUDING 10 10 HEME (COVALENT)
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Best Local Similarity
                                                                                    NCBI_TaxID=1083;
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P00086;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21128732; PubMed=11234002; James K.D., Thomson N.R., Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R. Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutherte S., Steyens K., Simon S., Simonds M., Skelton J., Squares R., Barrell B.G.;
                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=97124199; PubMed=8969512;
Fabih H., de Rossi E., Salazar L., Cantoni R., Labo M., Riccardi G., Takiff H.E., Eiglmeier K., Bergh S., Cole S.T.;
"Gene arrangement and organization in an approximately 76 kb fragment encompagasing the oric region of the chromosome of Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
-!- SIMILARITY: Belongs to the S6P family of ribosomal proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: Binds together with S18 to 168 ribosomal RNA (By
                                                                                  Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 21; DB 1; Length 96; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
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Ribosomal protein; FRNA-binding; Complete proteome.
SEQUENCE 96 AA; 10868 MW; CAA9C898F24B08C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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InterPro; IPR00529; Ribosomal_S6.
Fam; PF01250; Ribosomal_S6; 1.
ProDom; PD003809; Ribosomal_S6; 1.
IIGRPAMs; TIGR00166; S6; 1.
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EMBL; AL022118; CAA17954.1; --
EMBL; AL583926; CAC32217.1; --
PIR; C87245; C87445.
                  30S ribosomal protein S6.
RPSF OR ML2685 OR MLCB1913.21C.
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(Rel. 37, Last anno
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                                                               Mycobacterium leprae.
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=1769;
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21-JUL-1986
15-DEC-1998
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ID CY22 RHOMO
AC P00088;
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Query Match Matches

RESULT 12

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Gaps

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Length 100;

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TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN AND IS FOUND. IN SOME NONPHOTOSYNTHETIC BACTERIA.
HASP!, POOUNDS: IVEB.
InterPro: IPR003127; Cyt_CIAB.
InterPro: IPR003127; Cyt_CIAB.
InterPro: IPR003127; Cyt_CIAB.
PRINTS; PR00045; CYTCHRMECIAB.
PRINTS; PR000404; CYTCHRMECIAB.
PROSSITE; PS001905; CYTCHRMECIAB.
PROSSITE; PS001905; CYTCHRMECIAB.
PROSSITE; PS001905; CYTCHRMECIAB.
PROSSITE; PS001905; CYTCHRMECIAB.
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Submitted (JUN-1977) to the PIR data bank.
-!-FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR,
-!-FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR,
-!-FUNCTION: CYTOCHROME C2 IS FOUND TO THE BLOCTRON DONOR
TO THE OXIDIZED BACTERICCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION
PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN
AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA.

PIR; A00079; CCQPEM.
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Evolution of protein molecules, pp.311-322, Japan Scientific Societies
Press/Center for Academic Publications, Tokyo (1978).
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Rhodospirillum molischianum.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Rhodospirillaceae; Phaeospirillum.
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HEME (COVALENT).
IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
DECA12587457B0C2 CRC64;
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RON (HEME AXIAL LIGAND).

RON (HEME AXIAL LIGAND).

68FE59E2E3BF19D0 CRC64;
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Unpublished results, cited by:
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HEME (COVALENT).
IRON (HEME AXIAL I
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21.JUL-1986 (Rel. 01, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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InterPro; IPR003088; Cyt_CI.
InterPro; IPR003345; Cyt_CIAB.
InterPro; IPR003345; Cyt_CIAB.
Ffam; PF00034; Cytochrome_C; 1.
PRINTS; PR00604; CYTOCHNECIAB.
PRODOM; PD000375; Cyt_CIAB; 1.
PROSITE; P800190; CYTOCHROME_C; 1.
Electron transport; Photosynthesis; Heme.
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nes 4; Conservative
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P00087;
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*Incompared to the control of the control of the cytochrome c heme group can accept an electron from the heme group of the cytochrome c labbunit of cytochrome reductase. Cytochrome of the cytochrome clabbunit of cytochrome reductase. Cytochrome of the cytochrome cut then transfers this electron to the cytochrome oxidase complex, the final protein carrier in the mitochondrial electron-transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
-!- PTM: Binds 1 heme group per molecule.
-!- PTM: Binds 1 heme group per molecule.
-!- PTM: MISCELLUARBOUGS COMPARED CONTROL Cytochrome c's lacks one of the two cysteines that covalently bind the heme group.
-!- SIMILARITY: Belongs to the cytochrome c family.
PIR; A00004; URSJ.
InterPro; IPR00398; Cyt_CI.
InterPro; IPR00398; Cyt_CI.
InterPro; IPR00337; Cyt_CIAB.
InterPro; IPR0034; Cytochrome_C; I.
PEHM; PR00034; Cytochrome_C; I.
PRINTS; PR00044; CYTCHRMECIAB.
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000375; Cyt CIAB; 1.
PROSITE; PS00190; CYTOCHROME C; FALSE NEG.
Mitochondrion; Electron transport; Respiratory chain; Heme;
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HEME (COVALENT).
IRON (HEME AXIAL LIGAND).
IRON (HEME AXIAL LIGAND).
METHYLATION (TRI-).
W; 78414AD11EDA6F84 CRC64;
                                                                                                                                                                                                                                                                                                        Bukaryota, Buglenozoa, Buglenida, Buglenales, Buglena.
NCBL_TaxID=3039;
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100.0%; Pred. No. 2.8e+02;
tive 0; Mismatches 0;
            100.0%; Score 21; DB 1; 100.0%; Pred. No. 2.8e+02;
                                                                                                                                                                                                                         21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                            0; Mismatches
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18 18 IR
79 79 79 IRC
102 AA; 11210 MW;
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Best Local Similarity 100.0
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Query Match
Best Local Similarity 100...
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P00076;
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March 10, 2004, 08:58:54; Search time 1.24514 Seconds (without alignments) 309.015 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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21
1 GPSL 4
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1: pir1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ig mu chain V regi	3-mor	(L)			Ig heavy chain V r		ō.	CRF-related diuret	hypothetical prote	inorganic diphosph	myosin heavy chain	hypothetical prote	phosphoenolpyruvat	Ig heavy chain V r	hypothetical prote	NuMA protein - hum	NADH2 dehydrogenas	hypothetical prote		_	_	_	hypothetical prote	transcription regu	NADH2 dehydrogenas	NADH2 dehydrogenas	conserved hypothet	hypothetical 10.7K
SUMMARIES	ΙD	A43847	PN0583	PN0584	PN0585	PN0586	520771	C25159	SWLQDA	A48542	F90584	C38230	S35628	T31181	T03658	S36380	D70502	m	S01877	S.	T36853	0	B24853	B86780	D86861	C75296	JE0379	S28248	B69770	JQ2204
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CCQFF2 JC1195 C87245 PC4212	CCQFM2 D89861 CCQF2F	CCQF2M S14485 S14484 BR7208	CCEG S14486 S14487	S14488 H72609
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ALIGNMENTS

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A, Molecule type: genomic RNA
A, Realdues: 1-27 (ICH)
A, Caross-references: GB:114793
A, Experimental source: Iymph nodes
C, Comement: This enzyme catalyzes the first and rate-limiting step of catecholamine bios
C, Superfamily: phenylalanine 4-monooxygenase
C, Keywords: blopterin; monooxygenase; oxidoreductase
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C;Species: Bacillus subtilis
C;Species: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Dec-1998
C;Accession: C25159
R;Gaur, N.K.; Dubnau, E.; Smith, I.
J. Bacteriol. 168, 860-869, 1986
A;Title: Characterization of a cloned Bacillus subtilis gene that inhibits sporulation A;Reference number: A91827; MUID:87056981; PMID:3096962
A;Accession: C25159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig heavy chain V region (VH4, IN1P24) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 23-Jul-1999
C;Accession: $20771
R;Mortari, F.; Wang, J.; Schroeder, H.W.
R;Mortari, F.; Wang, Jota Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: $20764
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C.Species: Locusta migratoria migratorioides (African migratory locust)
C.Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 03-Nov-2003
C.Aacession: JH0244; S17864; A23702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-32 <MOR>
A;Residues: ESSE EMBL:211955; NID:933671; PIDN:CAA78012.1; PID:933872
A;Crose-referances: EMBL:211955; NID:933671; manunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Similarity 100.0%; Pred. No. 2.1e+02;
4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 21; DB 2; Length 27
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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A; Residues: 1-35 < GAU>
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A; Accession: PN0586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Molecule type: genomic RNA
A.Residues: 1-27 <ICH>
A.Cross-references: GB.14796
A.F.Experimental source: lymphocytes of peripheral blood
C.Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine blosy
C.Superfamily: phenylalanine 4-monooxygenase
C.Keywords: biopterin; monooxygenase; oxidoreductase
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A;Experimental source: lymphocytes of peripheral blood
C;Comment. This enzyme catalyzes the first and rate-limiting step of catecholamine biosy C;Superfamily: phenylalanine 4-monoxygenses
C;Keywords: biopterin; monooxygenase; oxidoreductase
                                                                                                                                                                                                           tyrosine 3-monooxygenase (EC 1.14.16.2) type 3 and 4 - gorilla (fragment)
Nylternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
C;Species: Gorilla gorilla (gorilla)
C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-2000
C;Accession: PNO584 #sequence_revision 07-Oct-1994 #text_change 31-Mar-2000
C;Accession: PNO584 #sequence_revision 07-Oct-1994 #text_change 31-Mar-2000
C;Accession: PNO584 #sequence_revision 07-Oct-1993
A;Title: Inoreased heterogeneity of tyrosine hydroxylase in humans.
A;Reference number: PNO575; MUID:93371398; PMID:7689834
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NiAlternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
C;Species: Hylobates lar (common gibbon, white-handed gibbon)
C;Accession: PNO586
R;Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
Biochem: Biophys. Res. Commun. 195, 158-165, 1993
A;Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A;Reference number: PNO575; MUID:93371398; PMID:7689834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine 3-monooxygenase (EC 1.14.16.2) type 3 and 4 - orangutan (fragment) NiAlbernate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase C;Species: Pongo pygmaeus (orangutan) C;Cpecies: 03-May-1994 #sequence_revision 07-0ct-1994 #text_change 31-Mar-2000
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Cyaccession: PNOSB:
R/Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
Biochem: Biochys. Res. Commun. 195, 188-186, 1993
A;Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A;Reference number: PNOS75; MUID:93371399; PMID:7689834
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100.0%; Score 21; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.78+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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Matches 4; Conserv
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Gaps

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A;Experimental source: strain UAB CTIP C;Genetics: A;Gene: MYPU 5820 A;Genetic code: SGC3

Ribehmberg, E.; Ota, R.B.; Furuya, K.; King, D.S.; Applebaum, S.W.; Ferenz, H.J.; School abothem. Blophye. Res. Commun. 179, 1036-1041, 1991
A;Title: Identification of a diuretic hormone of Locusta migratoria.
A;Reference number: JH0243; MUID:91378968; PMID:1654896

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myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: 835628
R;Babij, P.
Nucleic Acids Res. 21, 1467-1471, 1993
A;Title: Tissue-specific and developmentally regulated alternative splicing of a visce A;Reference number: 835628
A;Accession: 835628
A;Cross-references: EMBL:X70964; NID:q297108; PIDN:CAA50299-1; PID:g939958
C;Superfamily: myosin heavy chain; myosin motor domain homology
F;1-54/Domain: myosin motor domain homology (fragment) <MMOT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inorganic diphosphatase (EC 3.6.1.1) 1 - beet (fragments)
C;Species: Beta vulgaris (beet)
C;Species: Data vulgaris (beet)
C;Accession: C38230; B38230; F38230
R;Sarafian, V.; Kim, Y.; Poole, R.J.; Rea, P.A.
Proc. Natl. Acad. Sci. U.S.A. 89; 1775-1779; 1992
A;Title: Molecular cloning and sequence of CDNA encoding the pyrophosphate-cA;Reference number: A38230; MUID:92179265; PMID:1311852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: C38230
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Mocession: E38230
A; Mocession: E38230
A; Mote: sequence extracted from NCBI backbone (NCBIP:87192)
A; Mote: sequence extracted from NCBI backbone (NCBIP:87194)
A; Accession: F38230
A; Molecule type: protein
A; Residues: 29-52 cSAR3
A; Molecule type: protein
A; Residues: 29-52 cSAR3
A; Molecule type: protein
A; Residues: 29-52 cSAR3
A; Molecule extracted from NCBI backbone (NCBIP:87195)
C; Superfamily: H(+)-translocating inorganic pyrophosphatase
C; Keywords: hydrolase
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100.0%; Score 21; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 0;
                                                100.0%; Score 21; DB 2;
100.0%; Pred. No. 3e+02;
iive 0; Mismatches 0
                                                                                                                                      4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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S35628
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P90584

P90584

Pypotherical protein MYPU 5820 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C;Species: Mycoplasma pulmonis

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

C;Date: 24-May-2001 #sequence_revision 24-May-2001

R;Chacesion: P60584

R;Chambaud, I: Heilig, R.; Perris, S.; Barbe, V.; Samson, D.; Galisson, P.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A;Atitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUID:21267165; PMID:11353084

A;Atcession: P90584

A;Attaces preliminary

A;Attaces preliminary

A;Molecule type: DNA

A;Residues: 1-50 cKUR>

A;Residues: 1-50 cKUR>

A;Cross-references: GB:AL445566; PID:g1408997; PIDN:CAC13755.1; GSPDB:GN00153
A,Accession: JH0243
A,Molecule type: protein
A,Rolecule type: protein
A,Residues: 1-46 cLE2>
A,Experimental source: brain and corpora cardiaca
R;Kay, I.; Wheeler, C.H.; Coast, G.M.; Totty, N.F.; Cusinato, O.; Patel, M.; Goldsworthy
Bol. Chem. Hoppe-Seyler 372, 929-934, 1991
A,Title: Characterization of a diuretic peptide from Locusta migratoria.
A,Reference number: S17864; MUID:92126231; PMID:1663363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C. Accession: A48542

B.Kay, I.; Patel, M.; Coast, G.M.; Totty, N.F.; Mallet, A.I.; Goldsworthy, G.J.

B.Kay, I.; Patel, M.; Coast, G.M.; Totty, N.F.; Mallet, A.I.; Goldsworthy, G.J.

B.Goldston: Characterization and biological activity of a CRF-related diuretic I A; Reference number: A48542; MUID:93174045; PMID:1337794

A; Accession: A48542

A; Accession: Accession: A48542

A; Accession: A48542

A; Accession: Acce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Note: species designated as Locusta migratoria
C;Comment: This hormone stimulates urine production by Malpighian tubules and elevates
C;Superfamily: diuretic hormone, diuretic hormone homology
C;Keywords: amidated carboxyl end; diuretic; hormone; osmoregulation
F;2-46/Domain: diuretic hormone homology chem.
F;2-46/Domain: diuretic hormone homology chem.
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C;Species: Periplaneta americana (American cockroach)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 03-Nov-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Best Local Similarity 100.
Matches 4; Conservative
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A;Molecule type: protein
A;Residues: 1-46 <KAY>
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Best Local Similarity
Matches 4; Conserv
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23 GPSL 26

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Search completed: March 10, 2004, 09:16:43 Job time : 3.30396 secs
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R;Yanagisawa, S.; Izui, K.; Yamaguchi, Y.; Shigesada, K.; Katsuki, H.
FBBS Lett. 229, 107-110, 1998
A;Title: Further analysis of cDNA clones for maize phosphoenolpyruvate carboxylase involmENA at multiple sites in vivo.
A;Reference number: $600348; WUID:88152202; PMID:2894322
A;Accession: T03658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Description: catalyzes the irreversible beta-carboxylation of phosphoenolpyruvate by la parthway: carbon dioxide fixation C; Superfamily: phosphoenolpyruvate carboxylase C; Superfamily: phosphoenolpyruvate carboxylase C; Keywords: carbon dioxide fixation; carbon-carbon lyase; carboxy-lyase; phosphoprotein
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus susculus (house mouse)
C;Species: Mar-1997 #sequence_revision 29-Aug-1997 #text_change 23-Jul-1999
C;Accession: S36380; S33395
R;Ansell, K.H.
submitted to the EMBL Data Library, April 1993
A;Accession: S36380
A;Accession: S36380
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: Zea mays (maize)
Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL:X07171; NID:g22414; PIDN:CAA30159.1; PID:g929919 C; Function:
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Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 21; DB 2; Length 54; 100.0%; Pred. No. 3.2e.02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Scatus: preliminary; translated from GB/EMBL/DDBJ A;Nolecule type: mRNA A;Residues: 1-56 <YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                  A; Genome: plasmid pNL1
A; Note: orf505
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S36380
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A; Residues: 1-56 cANS.
A; Cross-references: BBL:X73008; NID:g295875; PIDN:CAAS1495.1; PID:g939938
B; Crettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Eur. J. Immunol. 23, 206-211, 1993
A; Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes us A; Reference number: S3391; MUID:93122032; PMID:8419173
A; Recession: S3395
A; Residues: 5-45 cKTT>
A; Cross-references: BMBL:X73008
A; Residues: 5-45 cKTT>
A; Cross-references: BMBL:X73008
C; Reywords: heterotetramer; immunoglobulin
C; Reywords: heterotetramer; immunoglobulin
F; 18-56/Domain: immunoglobulin homology (fragment) cIMM>
C; Reywords: heterotetramer; immunoglobulin cIMM>
C; Reywords: heterote
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652, App 258, App 258, Appl 25, Appl 27, Appl 27, Appl 27, Appl 28, Appl 29, Appl 31, Appl 31

Sequence Seq

OM protein

Run on:

Searched:

Database

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RESULT 1
US-09-848-834A-3
i Sequence 3, Application US/09848834A
i Sequence 3, Application US/09848834A
i Patent No. US20020056416A1
i GENERAL INFORMATION:
i APPLICANT: Aphton Corporation
i TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: 00/09/848,834A
i CURRENT FILING DATE: 2000-05-05
i PRIOR APPLICATION NUMBER: 60/202,328
i PRIOR APPLICATION NUMBER: 60/202,328
i NUMBER OF SEQ ID NOS: 20
i SOFTWARE: PatentIn version 3.0
i SEQ ID NO 3
i TYPE: PRT
i OKCANISM: Plasmodium falciparum
i FEBATURE:
i NAME/KEY: PEPTIDE
i COCTHER INFORMATION: Amino acid sequence 378-398 of the Plamodium
i OTHER INFORMATION: Amino acid sequence 378-398 protein
US-09-848-834A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
100.0%; Score 95; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e-0%;
Matches 20; Conservative 0; Mismatches 0; Indels
US-10-280-340-652
US-10-099-460-20
US-10-024-652-20
US-10-102-685A-25
US-10-102-685A-25
US-10-102-685A-25
US-10-1016-69-2
US-10-114-69-2
US-10-114-69-2
US-10-114-69-2
US-10-114-412-39
US-10-114-413-39
US-10-411-544-17
US-10-411-544-17
US-10-411-54-17
US-10-411-54-17
US-10-411-54-17
US-10-239-313A-36
US-10-239-313A-60
US-10-239-313A-65
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US-09-848-834A-12
Sequence 12, Application US/09848834A
; Patent No. US20020076416A1
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Sequence 12, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 54, Appl
Sequence 1482, Appl
Sequence 710, Appl
Sequence 711, Appl
Sequence 37, Appl
Sequence 761, Appl
Sequence 652, Appl
                                                                                   March 10, 2004, 09:16:59; Search time 15.7198 Seconds (without alignments) 268.645 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                     Published Applications AA:*

1. /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2. /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-848-834A.3
US-09-848-834A.12
US-09-848-834A.16
US-09-848-834A.20
US-09-848-834A.20
US-09-9313A-54
US-09-932-165-1482
US-09-942-052-711
US-10-001-469-1404
US-10-128-711-97
US-10-16-118-33
US-10-062-109A-761
US-10-052-109A-761
US-10-052-109A-761
US-10-291-2480A-761
US-10-291-2480A-761
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                809742 segs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                           - protein search, using sw model
                                                                                                                                    US-09-848-834A-3
95
1 DEKKIARMEKASSVFNVVNS 20
                                                                                                                                                                                      Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score: 9
Sequence:
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Gaps

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Score

Result No.

N

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OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human OTHER INFORMATION: GARH linked by a spacer to amino acid sequence 378-398 of Plasmo OTHER INFORMATION: ium falciparum circumsporozoite (CSP) protein NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (11)...(16)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (17)...(36)
OTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium falciparum
OTHER INFORMATION: circumsporozoite (CSP) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: PEPTIDE
LOCATION: (37)..(42)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (43)..(51)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1)...(10) OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
                                                                                                                                                                                                                                                                                                                                                                                Gaps
OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
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                        NAME/KEY: PEPTIDE

LOCATION: (11)..(16)

OTHER INFORMATION: Spacer peptide

LOCATION: (17)..(36)

OTHER INFORMATION: Amino acid sequence 378-398 of the Malaria
OTHER INFORMATION: (Plasmodium falciparum) circumsporozoite

US-09-848-834A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 95; DB 9; Length 51; Best Local Similarity 100.0%; Pred. No. 8e-08; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                  100.0%; Score 95; DB 9; Length 36; 100.0%; Pred. No. 5.5e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: (1) ...(1) OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline NAME/KEY: MOD RES LOCATION: (51)...(51) CATION: (51)...(51) Amidated glycine or glycinamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Aphen Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR APPLICATION NUMBER: 60/202,328
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-848-834A-20
; Sequence 20, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DEKKIAKMEKASSVFNVVNS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: PEPTIDE
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OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
LOCATION: (1)—(10)
                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 378-398 of the OTHER INFORMATION: Plasmodium falciparum CSP protein linked by a spacer to amino ac OTHER INFORMATION: id sequence 2-10 of the GnRH hormone

LOCATION: (1) ... (1)

OTHER INFORMATION: Amidated aspartic acid

NAME/KEY: MOD RES

LOCATION: (33)... (33)

OTHER INFORMATION: Amidated glycine or glycinamide
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CCATION: (25)..(33)
COTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone US-09-848-834A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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OTHER INFORMATION: Amino acid sequence 378-398 of the Malaria OTHER INFORMATION: (Plasmodium falciparum) circumsporozoite NAMEK INFORMATION: (CSP) protein LOCATION: (CSP) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 95; DB 9; Length 33;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 20; Conservative 0; Mismatches 0; Indels
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Patent No. US20020076416A1

GENERAL INFORMATION:

APPLICANT: Aphton Corporation

TILE OF INVENTION: Chimeric Peptide Immunogens

FILE REFERENCE: 1102865-0047

CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT APPLICATION NUMBER: 60/202,328

PRIOR PLING DATE: 2001-05-04

PRIOR PLING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Version 3.0

SOFTWARE: Patentin Version 3.0
                                  APPLICANT: Aphen Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047
FULE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: 05-04
FRIOR APPLICATION NUMBER: 60/202,328
FRIOR APPLICATION NUMBER: 60/202,328
FRIOR APPLICATION NUMBER: 2000-65-05
NUMBER OF SEQ ID NOS: 20
SEQ ID NOS: 20
SEQ ID NO 12
LENGTH: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (21)..(24)
OTHER INFORMATION: Spacer peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DEKKIAKMEKASSVFNVVNS 20
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                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                  SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-848-834A-16
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3 EKKIAKMEKASSVFNVVNS 21

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HUBBET, RENE
APPLICANT: HUBBET, RENE
APPLICANT: HUBBET, RENE
APPLICANT: RAIS, DANIEL
APPLICANT: LEVIN, ELANA
APPLICANT: LEVIN, ELANA
APPLICANT: GE, WANGWAO
TITLE OF INVENTION: UNCLEIC AND CORRESPONDING PROTEIN NAMED 158P1H4
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
TITLE OF INVENTION: USEFUL IN THE CANCERS
TITLE OF INVENTION: USEFUL IN CANCERS
TITLE OF INVENTION: USEFUL IN CANCERS
TITLE OF INVENTION: USEFUL IN VOO
CURRENT APPLICATION NUMBER: US/09/935,384
FILE REFERENCE: 51158-2003-08-22
PRIOR APPLICATION NUMBER: 60/227,098
PRIOR APPLICATION UNBER: 60/227,098
PRIOR APPLICATION UNBER: 60/227,098
PRIOR APPLICATION UNBER: 60/227,098
PRIOR SEQ ID NOS: 783
SOFTWARE PATENCE IN THE OF T
                                                                                                                                 US-09-935-384-710

Sequence 710, Application US/09935384

; Publication No. US20030166526A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-935-384-710
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ASPLICANT: CORVAIA.

Sequence 54, Application US/10239313A

Sequence 54, Application US/10239313A

Sequence 54, Application No. US20030175285A1

Sequence 54, Application No. US20030175285A1

GENERAL INFORMATION:

APPLICANT: KILINGUER. - HAWOUR, Christine

APPLICANT: CORVAIA, Nathalie

APPLICANT: CORVAIA, Nathalie

APPLICANT: GORNAIA, Nathalie

APPLICANT: GORNAIA, NATHALIE

TITLE OF INVENTION: MOLECTLE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS

TITLE OF INVENTION: NOT A PHYSICLOGICALLY ACCEPTABLE STRONG ACID

TITLE OF INVENTION: OR A PHYSICLOGICALLY ACCEPTABLE STRONG ACID

TITLE OF INVENTION: NUMBER: US/10/239,313A

CURRENT APPLICATION NUMBER: RR 00/03711

PRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 697

SOFTWARE: PATCHIN VEY: 2.1

SOFTWARE: PATCHIN VEY: 2.1
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Sequence 1462, Application WS.0932165

Publication No. US20030134784A1

GENERAL INFORMATION:
APPLICANT: RAITHAN, ARTHUR

APPLICANT: FARIS, MARY

APPLICANT: FARIS, MARY

APPLICANT: AFAR, DANIEL

APPLICANT: AF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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93.7%; Score 89; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 19; Conservative 0; Mismatches 0; Indels
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93.7%; Score 89; DB 10;

Best Local Similarity 100.0%; Pred. No. 2.6e-07;

Matches 19; Conservative 0; Mismatches 0;
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US-09-932-165-1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), ORGANISM: Plasmodium malariae US-10-239-313A-54
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LENGTH: 21
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US-09-942-052-711

i Sequence 711, Application US/09942052

publication No. US20030170626A1

GENERAL INFORMATION:
APPLICANT: Raitano, Arthur B.
APPLICANT: Farita, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rane S.
APPLICANT: Ge, Wangmao

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3

TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51188-20028.00

CURRENT FILING DATE: 2001-08-28

PRIOR FILING DATE: 2000-08-28

NUMBER OF SEQ ID NOS: 744

SEQ ID NO 711

LENGTH: 21
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  Length 21;
                                                 Indels
Query Match
93.7%; Score 89; DB 10; L
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 19; Conservative 0; Mismatches 0;
                                                                                                2 EKKIAKMEKASSVFNVVNS 20
                                                                                                                                      3 EKKIAKMEKASSVFNVVNS 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-942-052-711
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2 EKKIAKMEKASSVFNVVNS 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
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US-10-116-118-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-10-116-118-33
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JUS-10-011-469-1404

JUS-10-01-469-1404

JUS-10
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Publication No. US20030099634A1
GENERAL INFORMATION.
APPLICANT: VITIELLO, Maria A.
CHESTWOT, Robert W.
SETTE, Alessandro D.
CELIS, Esteban
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.7%; Score 89; DB 14; Length 21; Best Local Similarity 100.0%; Pred. No. 2.6e-07; Matches 19; Conservative 0; Mismatches 0; Indels
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COMPUTER READBLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIPICATION: vUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 EKKIAKMEKASSVFNVVNS 20
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                                    3 EKKIAKMEKASSVFNVVNS 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYPE: PRT
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-001-469-1404
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US-10-128-711-97
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Publication No. US20030143672A1
Fublication No. US20030143672A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn
APPLICANT: Ishioka, Glenn
APPLICANT: Ishioka, Glenn
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Softe, Alessandro
APPLICANT: Softe, Alessandro
APPLICANT: Softe, Alessandro
APPLICANT: Softe, Alessandro
FILE REFERENCE: 2060.0090003
CURRENT APPLICATION NUMBER: US 60/166,529
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Version 3.1
SEQ ID NO 33
LENGRIH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..21
OTHER INFORMATION: /note= "Malaria circumsporozoite 378-39" SEQUENCE DESCRIPTION: SEQ ID NO: 97:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 93.7%; Score 89; DB 14; Length 21; Best Local Similarity 100.0%; Pred. No. 2.6e-07; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.7%; Score 89; DB 14; Length 21; Best Local Similarity 100.0%; Pred. No. 2.6e-07; Matches 19; Conservative 0; Mismatches 0; Indels
APPLICATION NUMBER: US/08/197, 484
FILING DATE: 16-FEB-199
APPLICATION NUMBER: US 07/935,811
FILING DATE: 25-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-AUN-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/749,568
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REPERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELERA: (206) 623-6793
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
```

EKKIAKMEKASSVFNVVNS

```
Sequence 652, Application US/10277292

| Sequence 652, Application No. US2033199470A1
| Publication No. US2033199470A1
| GENERAL INFORMATION:
| APPLICANT: FARIS, MARY
| APPLICANT: HUBERT, RENE
| APPLICANT: ALTANO, ARTHUR
| APPLICANT: ALLIANA: ALLANA: APANICANT: CHALLITA-EID, PIA
| APPLICANT: CHALLITA-EID, PIA
| TITLE OF INVENTION: USEPUL IN THE TREATMENT AND DETECTION OF BLADDER AND
| TITLE OF INVENTION: UNBER: US/10/277,292
| CURRENT APPLICATION NUMBER: GO/227,098
| PRIOR PILING DATE: 2001-08-22
| PRIOR PELING DATE: 2000-08-22
| PRIOR PELING DATE: 2000-08-22
| PRIOR APPLICATION NUMBER: GO/227,098
| PRIOR PILING DATE: 2000-08-22
| PRIOR APPLICATION NUMBER: GO/227,098
| PRIOR PELING DATE: 2000-08-22
| PRIOR PELING DATE: 2000-08-22
| PRIOR APPLICATION NUMBER: GO/227,098
| PRIOR PELING DATE: 2000-08-22
| PRIOR PELING DATE: 2001-04-10
| NUMBER OF SEC ID NOS: 700
| SOFTWARE: PALENTH VAIR THE TREATMENT AND DETECTION UND GES
| LENGTH: 21
| LENGTH:
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APPLICANT: Aya Jakobovits
APPLICANT: Aya Jakobovits
APPLICANT: Arbur B. Raitano
APPLICANT: Arbur B. Raitano
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Rene S. Hubert
APPLICANT: Rene Meyrick Morrison
APPLICANT: Rene Meyrick Morrison
APPLICANT: Rene Meyrick Morrison
APPLICANT: Rene Jam Challita-Eid
APPLICANT: Rene Jam Challita-Eid
APPLICANT: Rene Jam Challita-Eid
APPLICANT: Rene Jam Challita-Eid
APPLICANT: Bia M. Challita-Eid
APPLICANTON: BYATILE Jam CHALE
APPLICANTION: BYATILE JOIN 10/291,241
CURRENT FILING DATE: 2003-03-18
FRIOR APPLICATION NUMBER: US 10/065,480
FRIOR APPLICATION NUMBER: US 60/282,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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; Sequence 26, Application US/10291241
; Publication No. US20030206905A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.7%; Sco
Best Local Similarity 100.0%; Pr
Matches 19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-277-292-652
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APPLICANT: Agensys
APPLICANT: Raiteno, Arthur B.
APPLICANT: Raiteno, Arthur B.
APPLICANT: Raiteno, Arthur B.
APPLICANT: Raiteno, Arthur B.
APPLICANT: Hubert, Rene S.
APPLICANT: Housert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer
FILE REPERENCE: 51158-20062.00
CURRENT PRILICATION NUMBER: US/10/005,480A
CURRENT FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 761
                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Agensys
APPLICANT: Agensys
APPLICANT: Raitano, Arthur B.
APPLICANT: Advending Force S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jokobovits, Aya
TITLE OF INVENTION: Builted 161P2F10B Useful in Treatment and Detection of
TITLE OF INVENTION: Cancer Cancer.
TITLE OF INVENTION: Cancer.
FILE REFERENCE: 51158-20662.01
CURRENT PAPLICATION NUMBER: US 10/005,480
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR PRING DATE: 2001-11-07
PRIOR PRING DATE: 2001-11-07
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FRIP
TYPE: PRT
TYPE: PRT

ORGANISM: Homo sapiens
US-10-062-109A-761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 89; DB 14; Length 21;
Pred. No. 2.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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93.7%; Score 89; DB
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                              RESULT 12
US-10-062-109A-761
US-10-062-105A-761
; Publication No. US20030165505A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 EKKIAKMEKASSVFNVVNS 20
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Best Local Similarity 100.
Matches 19; Conservative
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CRGANISM: Homo Sapien
US-10-005-480A-761
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels
) TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-291-241-26
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Search completed: March 10, 2004, 10:25:47 Job time : 15.7198 secs 2 EKKIAKMEKASSVFNVVNS 20 g

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model - protein search, using OM protein March 10, 2004, 08:58:54; Search time 6.22568 Seconds (without alignments) 309.015 Million cell updates/sec Run on:

US-09-848-834A-3 95 1 DEKKIAKMEKASSVFNVVNS Title: Perfect score: Sequence:

Scoring table:

283366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78: 4 2 2: pirt: * 4: pirt3: * 4: pirt4: * 4: pirt5: * 4: pirt7: * 4: pirt Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

circumsporozoite p	hypothetical prote	PTS betaglucoside-	conserved hypothet	F7H2.22 protein -
circumsporozoite p	membrane-associate	PTS betaglucoside-	probable transcrip	conserved hypothet
RhoGEF domain cont	hypothetical prote	conserved hypothet	phenylalanine tRNA	troponin I, fast s
C41156 A41156 T40088	T32958 H64701 D64317	559650 AF1121 AI1481 D82421	T40705 T50064 H81362	D86293 B82899 A31484
000	0000	1 11 11 11	000	000
387	627	4 4 4 C	563	921
395	175	1 4 4 C	708	442
525	333	2 4 4 C	773	201
444	4 4 4 4	4 4 4 4	4 4 4	4444
5.33	0 4 4 4	4 4 4 4	4 4 4	
5.33	6 0 0 0	7 6 6 6 6	5 6 7 7	
4 4 4	444	4 4 4 4	4 4 4	41.5
3 3 3	6000	7 4 4 4	0 0 0	41.5
0 E E	መመመር መቁጥላ	2 M M W W W W V	44 44 24 24	4 4 4 6 4 7

ALIGNMENTS

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AJS 758
Circumsporozoite protein - Plasmodium reichenowi
CiSpecies: Plasmodium reichenowi
AJS 756
Rilal, A.A.; Goldman, I.F.
J. Biol. Chem. 266, 6666-6689, 1991
A; Title: Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malari
A; Reference number: A39756; MUID: 91201303; PMID: 2016283
A; Accession: A39756
A; Accession: A39756
A; Molecule type: DNA
A; Residues: 1-388 < LAL
A; Residues: 1-388 < LAL
A; Residues: 1-388 < LAL
A; Crosser-references: GB: M60972; NID: 9160228; PIDN: AAA29561.1; PID: 9160229
C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F; 312-366/Domain: thrombospondin type 1 repeat homology < THRI>
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Gaps .. Length 388; Query Match 85.3%; Score 81; DB 2; Length 388 Best Local Similarity 89.5%; Pred. No. 4.7e-05; Matches 17; Conservative 0; Mismatches 2; Indels

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2 EKKIAKMEKASSVFNVVNS 20 셤 ઠે

356 EKKICKMEKCSSVFNVVNS 374

circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54)
Cispecies: Plasmodium falciparum
Cispecies: Portuge R45527; I60657
Ricampbell, J.R.
Nucleic Ardia Res. 17, 5854, 1989
A;Title: DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate v.
A;Reference number: S05428; MUID:89345189; PMID:2668895
A;Accession: 805428
A;Accession: 805428
A;Accession: Nos < CAM.
A;Residues: 1-405 < CAM.
A;Residues: 1-405 < CAM.
A;Residues: 1-405 < CAM.
A;Residues: 1-405 < CAM.
A;Reference number: A5527; MUID:89364998; PMID:2671723
A;Accession: 445527
A;Accession: 445527
A;Accession: A5527
A;Ac

A;Residues: 1-405 <CAS> A;Cross-references: GB:M22982; GB:J04650; NID:g160168; PIDN:AAA29527.1; PID:g160169 R;Lockyer, M.J.; Marsh, K.; Newbold, C.I.

(strain Wellcome)

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Gaps

. 0

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circumsporozoite protein precursor - Plasmodium berghei (strain NK65)

N;Alternate names: sporozoite surface antigen
C;Species: Plasmodium berghei
C;Species: 1980 modium berghei
C;Species: 1980 modium berghei
C;Accession: A44948; A25083; $13446

K;Funar, D.E.
Mol. Biochem. Parasitol. 39, 151-154, 1990
A;Title: Sequence of the circumsporozoite gene of Plasmodium berghei ANKA clone and NK6
A;Reference number: A44948; MUID:90158693; PMID:2406593
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C)Accession: A44969

R)Colomer-Gould, V.; Enea, V.

Mol. Biochem. Parasitol. 43, 51-58, 1990

A;Title: Plasmodium yoelii nigeriensis circumsporozoite gene structure and its implicat.

A;Reference number: A44969; MUID:91148645; PMID:2290446

A;Accession: A44969
                                                                                                                                                                                                                                          C. Accession: A54529
R.Lockyer, M.J.; Schwarz, R.T.
M.O. Blockyer, M.J.; Schwarz, R.T.
M.O. Blockyer, M.J.; Schwarz, R.T.
M.J. Schwarz, R.T.
M.J.; Schwarz, R.T.
M.J.; Schwarz, R.T.
M.J.; Schwarz, M.J.; Schwarz, R.T.
M. B. Hassiolo. 22, 101-108, 1987
M. Fitle: Strain variation in the circumsporozoite protein gene of Plasmodium falciparum A, Reference number: A54529
M. A. Accession: A54529
M. A. A. Conservation of compared with conceptual translation
M. M. Residues: 1-442
M. Conserve ference of Semissors, NID: g160214; PIDN: AAA29554.1; PID: g160215
C. Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C, Keywords: tandem repeat
F, 366-420/Domain: thrombospondin type 1 repeat homology < THRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-264 <COL>
A;Residues: 1-264 <COL>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;190-242/Domain: thrombospondin type 1 repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            circumsporozoite protein precursor - Plasmodium yoelii nigeriensis
C;Species: Plasmodium yoelii nigeriensis
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-Dec-1995
                                                                                                                            circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain C;Species: Plasmodium falciparum
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M28887
R;Eichinger, D.J.; Arnot, D.E.; Tam, J.P.; Nussenzweig, V.; Enea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Match
Local Similarity 89.5%; Pred. No. 5.4e-05;
les 17; Conservative 0; Mismatches 2; Indels
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Pred. No. 0.4;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EKKIAKMEKASSVFNVVNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 EKKIAKMEKASSVENVVNS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 DTEICKMDKCSSIFNIVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.98;
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Best Local Similarity 47.4
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate IMTM22)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jun-2000
C;Accession: A03388
R;Dame, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W.T.
Science 225, 593-599, 1984
A;Title: Structure of the gene encoding the immunodominant surface antigen on the sporoz
A;Title: Structure of the gene encoding the immunodominant surface antigen on the sporoz
A;Tocession: A03388
A;Molecule type: DNA
A;Residues: 1-412 cDAM>
A;Molecule type: DNA
A;Residues: 1-412 cDAM>
A;Cross-references: GB:X02194; NID:g160160; PIDN:AAA29524.1; PID:g160161
A;Experimental source: clone 7G8
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of the C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology <THRI>
F;336-390/Domain: thrombospondin type 1 repeat homology <THRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain 74, Thailand C;Species: Plasmodium falciparum alciparum falciparum falciparum falciparum falciparum falciparum falciparum falciparum falciparum falciparum fasces: Plasmodium falciparum fasces: Plasmodium falciparum fasces: Plasmodium falciparum fasces: Plasmodium falciparum faces: Plasmodium falciparum farasitol: 24, 289-294, 1987
A,Title: Circumsporozoite gene of a Plasmodium falciparum strain from Thailand. A,Reference number: A54533 MUID:87315205, PMID:3306373
A,Accession: A54533
A,Accession: A54533
A,Accession: A54533
A,Residues: 1-424 < DB.
A,Gross-references: GB.M19752; NID:9160216; PIDN:AAA29555.1; PID:9160217
C;Superfamily: circumsporozoite protein; thrombospondin type I repeat homology F;348-402/Domain: thrombospondin type I repeat homology
Mol. Biochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell ep
A;Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell ep
A;Reference number: A60657; MUID:90114334; PMID:2481827
A;Accession: 160657
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;329-383/Domain: thrombospondin type 1 repeat homology <THR1>
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 89.5%; Pred. No. 4.9e-05;
Matches 17; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 81; DB 2; Length 424
Pred. No. 5.1e-05;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 EKKICKMEKCSSVFNVVNS 398
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ilarity 89.5%;
Conservative C
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Best Local Similarity
Matches 17; Conserv
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circumsporozoite protein - Plasmodium malariae (strain Uganda 1-CDC)
C;Species: Plasmodium malariae
C;Species: Plasmodium malariae
C;Species: Plasmodium malariae
C;Species: Plasmodium malariae
C;Species: Oc-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 20-Aug-1999
C;Accession: A54504
R;Lal, A.A.; de la Cruz, V.F.; Campbell, G.H.; Procell, P.M.; Collins, W.E.; McCutchan A. Title: Structure of the circumsporozoite gene of Plasmodium malariae.
A;Title: Structure of the circumsporozoite gene of Plasmodium malariae.
A;Accession: A54504
A;Accession: A54504
A;Molecule type: DNA
A;Accession: A54504
A;Molecule type: DNA
A;Cross-references: GB:03392; NID:g160220; PIDN:AAA29557.1; PID:g160221
A;Cross-references: GB:03992; NID:g160220; PIDN:AAA29557.1; PID:g160221
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: tandem repeat
F;354-407/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aymolecule type: DNA
A;Residues: 1-367 <LAL>
A;Molecule type: DNA
A;Residues: 1-367 <LAL>
A;Cross-references: GBs.102695; NID:g160222; PIDN:AAA29558.1; PID:g160223
C;Comment: There are three distinct regions in the mature circumsporcacite protein, the obic membrane-anchoring sequence.
C;Comment: There are 15 copies of a 6-residue repeat and 8 copies of a 4-residue repeat C;Superfamily: circumsporcacite protein; thrombospondin type 1 repeat homology C;Reywords: sporcacite; surface antigen; thrombospondin type 1 repeat homology C;Reywords: sporcacite protein #status predicted <NG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;139-228/Region: 6-residue repeats (Q-G-P-P)
F;229-260/Region: 4-residue repeats (Q-O-P-P)
F;293-345/Domain: thrombospondin type 1 repeat homology <THRI>
                                                                                                                                                                                                                                                                       C,Accession: A26271
R,Lal, A.A.; de la Cruz, V.F.; Welsh, J.A.; Charcenvit, Y.; Maloy, W.L.; McCutchan, T. J. Biol, Chem. 262, 237-2340, 1987
A; Title: Structure of the gene encoding the circumsporozoite protein of Plasmodium yoe A; Reference number: A26271; MUID:87137555; PMID:3102479
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circumsporozoite protein precursor - Plasmodium brasilianum
circumsporozoite protein prasilianum
cispecies: Plasmodium brasilianum
cispecies: Plasmodium brasilianum
cispecies: Plasmodium brasilianum
cispate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
CiAccession: A60610; A28615
Ryid Giovanni, L.; Cochrane, A.H.; Enea, V.
Bxp. Parasitol. 70, 373-381, 1990
A;Title: On the evolutionary history of the circumsporozoite protein in plasmodia.
A;Reference number: A60610; MUID:90214818; PMID:2323391
                                                                               circumsporozoite protein precursor - Plasmodium yoelii
N;Alternate names: sporozoite surface antigen
C;Species: Plasmodium yoelii
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.9%; Score 55; DB 1; Length 367; Best Local Similarity 47.4%; Pred. No. 0.56; Matches 9; Conservative 7; Mismatches 3; Indels
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Best Local Similarity 47.4.
Best Local 9, Conservative
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                                                                                              A;Nolecule type: DNA
A;Residues: 1-26, II,28-68, PMLRR',75-126, P',128-134, PPPNANDP',135-332 <EIC>
A;Cross-references: GB.M14135, NID:g160245, PIDN:AAA39577 1; PID:g160246
R;Neber, JL.; Bgan, J.B.; Lyon, J.A.; Wirtz, R.A.; Charoenvit, Y.; Maloy, W.L.; Hockmey
Exp. Perasitol. 63, 295-306, 1987
A;Title: Plasmodium berghei: cloning of the circumsporozoite protein gene.
A;Accession: 813446; MUD:87218962; PMID:3556207
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A,Title: Circumsporozoite protein of Plasmodium berghei: gene cloning and identification
A,Reference number: A25083, MUID:87089740, PMID:2432395
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N;Alternate names: sporozoite surface antigen
C;Species: Plasmodium berghei
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A;Residues: 1-59,1', 61-81,83-348 <LOC2>
A;Cross-references: EMBL:X17606; NID:g9784; PIDN:CAA35608.1; PID:g9785
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999 C.Accession: S07873, S12571 R.Lockyer, M.J.; Davies, C.S.; Suhrbier, A.; Sinden, R.E. Nucleic Acids Res. 18, 376, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Best Local Similarity 47.4%; Pred. No. 0.51;
Matches 9; Conservative 7; Mismatches 3; Indels
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F;274-326/Domain: thrombospondin type 1 repeat homology <THR1>
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721-348/Product: circumsporozoite protein #status predicted
794-205/Region: 8-residue repeats
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Lockyer, M.J.
submitted to the EMBL Data Library, November 1989
A;Referen number: S12571
A;Accession: S12571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 DTEICKMDKCSSIFNIVSN 318
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Conservative
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A; Residues: 1-348 <LOC>
A; Cross-references: EMBL:X17606
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les 9, Conserv
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Best Local S:
Matches 9
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Circumsporozoite protein precursor - Plasmodium cynomolgi (strain London)
NiAlternate names: major sporozoite surface antigen
Cispecies: Plasmodium cynomolgi
Cispecies: Plasmodium cynomolgi
Cjacesion: A2625
RACCESION: A2625
RAGalinski, M.R., Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Enea, R; Refarence number: Apo889; MUD:87102878; PMID:3802196
A; Reference number: A90889; MUD:87102878; PMID:3802196
A; Reference number: A90889; MUD:87102878; PMID:3802196
A; Residues: 1-378 cdAL.
C; Comment: There are three distinct regions in the mature circumsporozoite protein, the objc membrane-anchoring sequence. Comment: There are 19 tandem copies of a 6-residue repeat and 6 copies of an 11-resid C; Superfamily: circumsporozoite protein; thromobospondin type I repeat homology C; Superfamily: circumsporozoite protein; tandem repeat
C; Superfamily: circumsporozoite protein; thromobospondin type I repeat homology C; Reywords: sporozoite; surface antigen; tandem repeat
C; Superfamily: circumsporozoite protein; phasen: are a predicted & SIGS
C; Parodiure: Circumsporozoite protein; phasen: are a predicted & SIGS
C; Superfamily: circumsporozoite protein; phasen: are a predicted & SIGS
C; Superfamily: circumsporozoite protein; phasen: are a predicted & SIGS
C; Superfamily: circumsporozoite protein; phasen: are a predicted & SIGS
C; Superfamily: circumsporozoite protein; phasen: are a predicted & SIGS
C; Superfamily: circumsporozoite protein; phasen: a predicted & SIGS
C; Superfamily: circumsporozoite protein; phasen: a predicted & SIGS
C; SIGNOSOITE & 
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A) Residuate: 1-398 (GAL)

C) Comment: There are three distinct regions in the mature circumsporozoite protein, the cobic membrane-anchoring sequence.

C) Comment: There are 16 tandem copies of a 9-residue repeat and 3 copies of a 17-residu c) Superfamily: circumsporozoite protein, thrombospondin type 1 repeat homology C) Reywords: sporozoite; surface antigen; tandem repeat c) Reywords: sporozoite; surface antigen; tandem repeat product: circumsporozoite protein #status predicted <NIC>
F):1-19/Domain: signal sequence #status predicted <NIC>
F):97-240/Region: 9-residue repeats
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology C;Keywords: sporozoite; surface antigen; tandem repeat F;1-19/Domain: signal sequence #status predicted <SIG>F;20-378/Product: circumsporozoite protein #status predicted <MAT>F;97-192/Region: 9-residue repeats F;193-268/Region: 16-residue repeats F;193-268/Region: thrombospondin type 1 repeat homology <THRI>
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NyAlernate names: major sporozoite surface antigen
C;Species: Plasmodium cynomolgi
C;Species: Plasmodium cynomolgi
C;Species: Plasmodium cynomolgi
C;Date: 30-Sep.1987 #sequence_revision 30-Sep.1987 #text_change 07-Nov-1997
C;Accession: C26255
R;Galinski, M.R; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig,
A;Galinski, M.R; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig,
A;Tile: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A;Reference number: A90889; MUID:87102878; PMID:3802196
A;Accession: C26255
A;Molecule type: DNA
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F;212-277/Region: 11-residue repeats
F;303-356/Domain: thrombospondin: type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                           DB 1; Length 378; 22;
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                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 22;
7; Mismatches
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nes 7; Conservative
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Matches 7; Conserv
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A,Residues: 1-378 <GAL>
C,Comment: There about three distinct regions in the mature circumsporozoite protein, the
objc membrane-anchoring sequence.
C,Comment: There are 10 tandem copies of a 9-residue repeat (preceded by a 6-residue ind
                                                                                                      A; Molecule type: DNA
A; Residues: 1-485; Calb.
A; Residues: 1-485; Calb.
A; Residues: 1-485; Calb.
A; Residues: 1-485; Calb.
A; Residues: 1-485; Cals.
A; Residues: 1-485; Cals.
A; Title: Circumsporozoite protein gene from Plasmodium brasilianum. Animal reservoirs for A; Reference number: A28615; MUD:88186854; PMID:3128542
A; Reference number: A28615; MUD:88186854; PMID:3128542
A; Residues: 93-485 clal.
C; Reywords: sporozoite protein; thrombospondin type 1 repeat homology
C; Reywords: sporozoite surface antigen; tandem repeat
C; Reywords: sporozoite squence afstatus predicted class
F; 1-485 forduct: circumsporozoite protein #status predicted class
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NyAlternate names: major sporozoite surface antigen
C;Species: Plasmodium cynomolgi
C;Species: Plasmodium cynomolgi
C;Accession: D26258
R;Galinski, M.R.; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, IG11 48, 311-319, 1987
A;Ftle: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A;Reference number: A90889; MUID:87102878; PMID:3802196
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C;Species: Canis lupus familiaris (dog)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-1534 «WAN»
A;Cross-references: GB:X87224; NID:g984113; PIDN:CAA60676.1; PID:g984114
C;Keywords: endoplasmic reticulum; membrane protein; protein biosynthesis
P;198-743/Region: 10-residue repeats (N-Q-G-K-K-A-E-G-A-P)
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Sylanker, E.B.; Sun, Y.; Savitz, A.J.; Meyer, D.I.
J. Cell Biol. 130, 29-39, 1995
A;Title: Functional characterization of the 180-KD ribosome receptor in A;Reference number: A56734; MUID:95310363; PMID:7790375
A;Status; preliminary; not compared with concentral transfer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;21-485/Product: circumsporozoite protein #status predicted c: F;114-369/Region: 4-residue repeats
F;410-463/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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Pred. No. 68;
                                                              Status: not compared with conceptual translation
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EKKVAKVEPA--VSSVVNS 159
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453 ETEICSLDKCSSIFNVVSN 471
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ilarity 63.2%;
Conservative 3
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Best Local Similarity 47.4%
Best Local 9; Conservative
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Best Local Similarity
Matches 12; Conser
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| Sequence 3, Application US/09810601
| Patent No. US20020177545A1
| GENERAL INFORMATION: Stephen | APPLICANT: Donovan, Stephen | TITLE OF INVENTION: Composotions and Methods for Treating Gonadotrophin | TITLE OF INVENTION: Composotions and Methods for Treating Gonadotrophin | TITLE OF INVENTION: Related Illnesses | FILE REFERENCE: 2947 | CURRENT APPLICATION NUMBER: US/09/810,601 | CURRENT FILING DATE: 2001-03-15 | NUMBER OF SEQ ID NOS: 44 | SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09810601

Patent No. US20020177545A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Composotions and Methods for Treating Gonadotrophin TITLE OF INVENTION: Related Illnesses
TITLE REPERENCE: 2947
CURRENT APPLICATION NUMBER: US/09/810,601
CURRENT APPLICATION NUMBER: US/09/810,601
CURRENT FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 2
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description of Artificial Sequence: Gonadotrophin Release Hormone Analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gonadotropy OTHER INFORMATION: Release Hormone Analogue
NAME/KEY: MOD_RES
I.OCATION: (1)
OTHER INFORMATION: Xaa at position 1 is PyroGlu;; PYRROLIDONE
OTHER INFORMATION: CARBOXYLIC ACID
NAME/KEY: MOD_RES
I.OCATION: (10)
OTHER INFORMATION: Xaa at position 10 is Gly-NH2; AMIDATION;
PUBLICATION: NIFORMATION: Xaa at position 10 is Gly-NH2; AMIDATION;
PUBLICATION INFORMATION:
PUBLICATION DATE: 1993-07-07
PUBLICATION INFORMATION:
AUTHORS: Rousselle, Ghristophe
JOURNAL: MOI. Pharmacol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                     DB 9; Length 10; 0.022;
                                                                        Query Match

96.3%; Score 52; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 8; Conservative 0; Mismatches
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OTHER INFORMATION: CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 8; Conservative
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US-09-810-601-1

Sequence 1, Application US/09810601

Fatent No. US20020177545A1

GENERAL INFORMATION:

APPLICANT: Donovan, Stephen

TITLE OF INVENTION: Composcitions and Methods for Treating Gonadotrophin

TITLE OF INVENTION: Related Illnesses

FILE REFERENCE: 2947

CURRENT APPLICATION NUMBER: US/09/810,601

CURRENT FILING DATE: 2001-03-15

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.1
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NAME/KEY: MOD_RES
NAME (1)
OTHER INFORMATION: Xaa at position 1 is PyroGlu; PYRROLIDONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.3%; Score 52; DB 9; Length 10; 100.0%; Pred. No. 0.022; tive 0; Mismatches 0; Indels
                                                                                                                                                                                  96.3%; Score 52; DB 9; Length 10; 100.0%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCATION: (1) ... (1)
COTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
NAME/KEY: MOD RES
LOCATION: (10) ... (10)
COTHER INFORMATION: Maidated-glycine or glycinamide
US-09-848-834A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVEXTION: Chineric Peptide Immunogens
CURRENT PAPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
PRIOR PILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 1
LENGTH: 10
TYPE: PRI
CRANISM: Homo sapiens
                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09848834A Patent No. US20020076416A1 GENERAL INFORMATION:
        SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-019-010-2
                                  : 10 amino acids
amino acid
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-848-834A-1
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Sequence 17, Appli Sequence 17, Appli Sequence 3, Appli Sequence 4, Appli Sequence 1146, Ap Sequence 1177, Ap Sequence 1173, Ap Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appl Sequence 31, Appl Sequence 1145, Ap Sequence 1145, Ap Sequence 1145, Appl Sequence 1145, Appl

Sequence 1309, Ap Sequence 1344, Ap Sequence 13, Appli Sequence 23, Appli Sequence 1, Appli Sequence 5, Appli Sequence 3, Appli

```
Sequence 2, Application US/09019010
Patent No. US20010014330A1
GENERAL INFORMATION:
APPLICANT: HARLAND:
APPLICANT: ACRES, STEPHEN D.
TITLE OF INVENTION: IMMUNIZATION AGAINST ENDOGENOUS
TITLE OF INVENTION: MOLECULES
NOMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENDING PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FURM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
SOSTEM: PatentIn Release #1.0, Version #1.30
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 60/036,883
CLASSIFICATION NUMBER: US 60/036,883
FILING DATE: 05-FEB-1997
ATTOREY AGENT INFORMATION:
NAME: MCCRACKEN, THOMAS P.
REGISTRATION NUMBER: 9001-0035
TELEPHONE: (650) 325-7812
TELEPHONE: (650) 325-7812
TELEPHONE: (650) 325-7823
INFORMATION FOR SEQ ID NO: 2:
US-10-351-641-1143

US-10-351-641-1349

US-10-351-641-1349

US-10-170-096A-23

US-10-360-101-19

US-10-360-101-29

US-10-360-101-29

US-10-360-101-19

US-10-298-378-1

US-10-298-378-1

US-10-298-378-1

US-10-298-378-1

US-10-298-378-1

US-10-298-378-1

US-10-298-378-1

US-10-298-378-1

US-10-31-641-1146

US-10-351-641-1172

US-10-351-641-1173

US-10-351-641-1173

US-09-964-201A-26

US-09-964-201A-26

US-09-964-201A-26

US-09-964-201A-26

US-09-964-201A-27

US-10-351-641-1145

US-10-351-641-1145

US-10-351-641-1145
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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US-09-019-010-2
      Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 32, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
                                                                                                        March 10, 2004, 09:16:59 ; Search time 7.85992 Seconds (without alignments) 268.645 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

(cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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(cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

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(cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*)
                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                  809742 segs, 211153259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                     US-09-848-834A-1
54
1 XHWSYGLRPX 10
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Match
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                                                                                                                                                                                                                                      Scoring table:
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No.
                                                                                                             Run
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Location/Qualifiers

/label= Gly-NH2

/label= Pyr

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Key
Misc-difference
                             Modified-site
                                                                                  24-AUG-1981
                                                             BE887639-A.
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80US-00152241 80US-00152241

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Gonadorelin for treatment of benign prostatic hyperplasia - is the deca:peptide Pyr-His-Trp-Ser-Tyr-Gly-Leu-Arg-Pro-Gly-nh2 or luteinising hormone.
                                                                             (AMHP ) AYERST MCKENNA & HARRISON LTD.
                                                                                                                                      Claim 1; Page 7; 9pp; French.
                                                                                                    WPI; 1981-66067D/37.
                                                       22-MAY-1980;
                                                                  22-MAY-1980;
                                                                                        Auclair C;
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The inventors claim a compsn. for the redn. or prevention of undesired prostatic growth in males. The compsn. contains a decapeptide (gonadorelin) (AAP10097) with an appropriate vehicle or support. The compsn. is used for treating e.g. benign prostatic hyperplasia by parenteral admin. in daily doses of 0.035-11.0 (pref. 0.080-2.0) mg/kg. Gonadorelin is the generic name for LH-RH and is described in US3835108. In the example s.c. injection of the compsn.significantly reduced the wt. of seminal vesicles and ventral prostate in rats without affecting the wt. of the testicles. (Updated on 25-MAR-2003 to correct PA field.) Sequence 10 AA;

0; Gaps 96.3%; Score 52; DB 1; Length 10; 100.0%; Pred. No. 0.0078; tive 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 8; Conservative

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2 HWSYGLRP 9

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HWSYGLRP 9

Search completed: March 10, 2004, 09:12:00 Job time : 18.0584 secs

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composition is used to treat prostate adenocarcinoma, benign hypertrophy of the prostate, endometriosis, dysmenorrhea, hirsutism, hormonedependent mammary tumours, for treatment or prevention of precocious puberty, delaying the onest of puberty and for treating acne. The compositions may also contain antiandrogens. See also AAP10412-P10418. (Updated on 01-UUL-2002 to add missing PI field.) (Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LH-RH, liberating factor for LH and FSH, and its agonists compsn. - used to treat prostate adenocarcinoma, benign hypertrophy of the prostate, hirsutism, acne, etc.
                                            LHRH; Follicle Stimulating Factor; FSH; acne; hirsutism; dysmenorrhea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of luteinising hormone (LH-RH, ICSH) liberating hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gonadorelin, luteinising hormone releasing hormone; LH-RH; ICSH; prostatic hyperplasia therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A composition is claimed containing LHRH or its analogues. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                           precocious puberty; endomētriosis; prostate cancer; benign prostate hypertrophy; mammary tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; L 0.0078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%; Score 52; DB 100.0%; Pred. No. 0.C
                                                                                                                                                                              /label= OTHER
/note= "pyroglutamic acid"
                Luteinising Hormone Releasing Hormone.
                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1(a); Page 15; 27pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP10097 standard; peptide; 10 AA.
                                                                                                                                                                                                                                /note= "amidated"
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                    (ROUS ) ROUSSEL-UCLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                      Labrie F, Raynaud J;
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                   21-SEP-1979;
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19-AUG-1992
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                                                                                                                                                                                                                                                                    BE885308-A.
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                                                                                                                 Mammalia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A composition is claimed containing LHRH or its analogues. The composition is used to treat prostate adenocarcinoma, benign hypertrophy det the prostate, endometriosis, dysmenorrhea, hirsutism, hormone-dependent mammary tumours, for treatment or prevention of precocious puberty, delaying the onset of puberty and for treating acne. The compositions may also contain antienadrogens. See AAPIU411-P10411. (Updated on 01-UUL-2002 to add missing PI field.) (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - used
                                                                                                                                                                                                                                                                                                                                   note= "amidated or absent, in which case Pro(9) is Pro-
                                                                           LHRH; Follicle Stimulating Factor; FSH; acne; hirsutism; dysmenorrhea; precocious puberty; endometriosis; prostate cancer; benign prostate hypertrophy; mammary tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LH-RH, liberating factor for LH and FSH, and its agonists compsn. - u to treat prostate adenocarcinoma, benign hypertrophy of the prostate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                Luteinising Hormone Releasing Hormone analogue #5
                                                                                                                                                                                                                                                                                                      note= "N-alpha-methyl-Leu"
                                                                                                                                                                                                                                                    'note= "pyroglutamic acid"
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1(f); Page 16; 27pp; French.
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                                                                                                                                                                                                                                  label= OTHER
                                                                                                                                                                                                                                                                                      label= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Labrie F, Raynaud J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to treat prostate ade
hirsutism, acne, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1981-23409D/14.
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Modified-site
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10-MAR-2003
01-JUL-2002
17-DEC-1992
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 01-JUL-2002
17-DEC-1992
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Gaps

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Indels

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Pred. No. 1.4 Mismatches

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The invention relates to an agent comprising a neurotoxin preferably botulinum toxin for treating endocrine disorders for e.g. gonadotrophin related illness. The agent is useful for treating gonadotrophin related illness e.g. prostate cancer, endometrial cancer, pancreatic cancer, breast cancer, endometrions or precocious puberty. It is also useful for decreasing gonadotrophin secretion in a mammal. The present sequence is gonadotrophin releasing hormone analogue (GnRH-A)
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antihyperlipaemic; antithrombotic and/or anticancer agent or an agent for treating menopause. The composition of the invention is useful for treating and preventing diseases associated with angiotensin II, such as: circulatory diseases; hypertension; gastrointestinal disorders and cancer. The present amino acid sequence is used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                        Gonadotrophin releasing hormone analogue, neurotoxin; prostate cancer; endocrine disorder; gonadotrophin related illness; endometrial cancer; pancreatic cancer; breast cancer; endometriosis; precocious puberty;
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                                                                                                                                                                   Gaps
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                                                                                                                                                                   Indels
                                                                                                                                        Length 9;
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1. 1.4e+06;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Pyroglutamic acid"
9
                                                                                                                                                                      Mismatches
                                                                                                                                        96.3%; Score 52;
100.0%; Pred. No.
iive 0; Mismatc
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                                                                                                                                                                                                                                                                                                         AAE29840 standard; peptide; 9 AA
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                                                                                                                                                                    Conservative
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                                                                                                                                                        Local Similarity
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                                                                                                              Sequence 9 AA;
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                                                                                 the invention
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Matches
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Length 9;

DB 6;

Score 52;

96.3%;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agent for preventing post-operative recurrence of premenopausal breast cancer contains GnRH agonists or antagonists.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                      releasing hormone agonist; GnRH agonist; cancer; breast cancer; cytostatic.
                                                                                                                                                                                 Gonadotrophin releasing hormone agonist peptide gonadrelin.
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Pred. No. 1.4e+06;
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9
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100.0%; Pre
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 Similarity 100.
8; Conservative
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Best Local Similarity
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                                  2 HWSYGLRP
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                                                                                                                                                                                                           Gonadotrophin
premenopausal
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Modified-site
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10-MAR-2003
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Best Local S
Matches
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04-AUG-2003 (first entry)
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                     2 HWSYGLRP 9
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                                                                                                                                                                                     Sequence 9 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                       The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a cadtive group (II) (e.g. succilimidy! and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a ceptidase stabilised therapeutic peptide composed of 3.50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth contransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not sultable as drug candidates as they require frequent compities are not sultable as drug candidates as they require frequent compities are not sultable as drug candidates as they require frequent contradiction due to rapid degradation by peptidases in the body. Contradiction of peptidases to increase length of activity (half contradellular uptake and interference with physiological processes. AAB30829 to AAB32441 represent peptides which can be used in the case applification of the present invention
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                                                    Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GnRH-III; autoimmune disease; transplant rejection; retroviral disease; graft-versus-host-disease; lymphoproliferative disease; gonadotropin-releasing hormone.
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         Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                 96.3%; Score 52; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06; cive 0; Mismatches 0; Indels
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         Holmes DL,
                                                                                     Disclosure; Page 238; 733pp; English.
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         Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB59836 standard; peptide; 9 AA.
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          Ezrin AM,
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                               WPI; 2001-112059/12
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les 8; Conserv
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB59836;
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The present invention relates to a product comprising a proliferatively active moiety (PAM) linked to nucleic acid material which is associated with a protective material. The PAM product is useful for manufacturing a medicament for treating e.g. an autoimmune disease, transplant rejection, retroviral disease, graft-versus-host-disease, or lymphoproliferative disease, comprising cells bearing a high affinity receptor for PAM. The present sequence is a peptide of gonadotropin-releasing hormone (GnRH). GnRH is a peptide hormone, which has high-affinity receptors, and therefore can be used in the present invention
Novel product comprising proliferatively active moiety linked to genetic material, useful as vectors for protected nucleic acid material and as mitogen to stimulate proliferation of target cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Pyro glutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 37; 120pp; Japanese.
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                                                                                                                                                                                       Disclosure; Page 4; 49pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO16785 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-AUG-2001; 2001JP-00236794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-2002; 2002WO-JP007862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TAKE ) TAKEDA CHEM IND LTD.
(KAWA/) KAWAMURA R.
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(CONJ-) CONJUCHEM INC
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10-SEP-1999;
15-OCT-1999;
       17-MAY-1999;
10-SEP-1999;
15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-2000.
                                                                  Bridon DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB90972;
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                             셤
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                                                                                                                                                                                                                                                                                                             The present sequence represents luteinising hormone releasing hormone (LHRH). It is used in vaccines with T helper cell epitopes AAB08076-B08101, derived from canine distemper virus (CDV). Compositions comprising these T cell helper epitopes are useful for inducing an immune response in an animal. The epitopes are useful as components of animal, in particular, canine vaccines, either simply as synthetic peptide based vaccines and as additions to vaccines containing more complex antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Luteinising hormone releasing hormone (LH-RH) related peptide SEQ ID:153.
                                                                                                                                                                                                                                                                 Novel T helper cell epitopes derived from canine distemper virus useful for preparation of canine vaccines.
         Amino acid sequence of truncated luteinising hormone releasing hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl; maleimido group, amino, hydroxyl; thiol; hormone, growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                   .
                           T helper cell epitope; CDV; immune response; canine vaccine;
luteinising hormone releasing hormone; LHRH.
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                96.3%; Score 52; DB 3; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0;
                                                                                                                                                                          (CSLC-) CSL LTD.
(CSLR.) COMMONWEALTH SCI & IND RES ORG.
(COUN-) COUNCIL QUEENSLAND INST WEDICAL RES.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                          Walker J;
                                                                                                                                                                                                                                                                                              Example 3; Page 21; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB90979 standard; peptide; 9 AA.
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                                                                                                                  07-FEB-2000; 2000WO-AU000070.
                                                                                                                                    99AU-00008533
99AU-00002013
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                           Souravi G,
                                                                                                                                                                 (UYME ) UNIV MELBOURNE.
                                                                                                                                                                                                                                               WPI; 2000-532904/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 HWSYGLRP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HWSYGLRP
                                                                           WO200046390-A1.
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
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                                                                                                                                     05-FEB-1999;
04-AUG-1999;
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                                                                                              10-AUG-2000
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                                                          Canis sp.
                                                                                                                                                                                                                           Jackson
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The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a

comprising a therapeutically active amino acid region (III) and a tracthed to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a compared set all therapeutic peptide composed of 3.50 amino acids.

Comprision and neurotransmitters, to protect them from peptides activity in two factors and neurotransmitters, to protect them from peptides activity in compared to the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent complication due to rapid degradation by peptidases in the body.

Comprision and actaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half compared in the present physiological processes.

Compared to the present invention compared in the compared to the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Luteinising hormone releasing hormone (LH-RH) related peptide SEQ ID:146.
                                                                                                                                                                                                                                                                                                                              Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl, thiol, hormone, growth factor, neurotransmitter.
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                                                                                                                                                                                            Thibaudeau K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.3%; Score 52; DB 4; Le
100.0%; Pred. No. 1.4e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                            Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 240; 733pp; English
                                                                                                                                                                                            Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB90972 standard; peptide; 9 AA.
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99US-0153406P.
99US-0159783P.
99US-0134406P.
99US-0153406P.
99US-0159783P.
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Query Match
Best Local Similarity 100.vv.
Bervative
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                                                                                                                                 (CONG-) CONJUCHEM INC
                                                                                                                                                                                                   Ezrin AM,
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The invention relates immunogenic composition for eliciting an immune response to lutainising hormone releasing hormone (LHRH). The composition response to lutainising hormone releasing hormone (LHRH). The composition computates a LHRH-diphtheria toxoid (UT) conjugate adsorbed to an ionic comprises a LHRH-diphtheria toxoid in an ionic confirmation of an animal of carefulating obstruction of an animal, e.g. aggression or sexual activity. They can also be used for achieving production gains in livestock by the sexual maturation of an animal, e.g. aggression or sexual activity. They can also be used for inhibiting the growth of cells which are regulated directly or indirectly by LHRH, e.g. malignant broated cells, malignant ovarian cells, malignant concerts cells, malignant or hyporphisatic cells. They can also be used for inhibiting pregnancy, prostate cells, malignant confidence of an animal. They can also be used for down-regulating the libido of an animal. They can also be used for inhibiting pregnancy, prostate enlargement, endomerricals or inflammatory responses. The LHRH compositions induce a more effective immune response against LHRH than the LHRH-carrier-adjuvant compositions. The effective immune response against LHRH are allers in prevention of the release of the hormones LH and PSH from the anterior pituitary. Sequences AAW94890-93 care peptide derivatives of LHRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic leutenising hormone releasing hormone compositions -comprise LHRH conjugated to diphtheria toxoid and adsorbed to an ionic polysaccharide, used to inhibit reproductive function in animals.
                                                                                                                                                                                                                                                                                                                                                LHRH; immune response; luteinising hormone releasing hormone; DT; diphtheria toxoid; castrating; oestrus cycling; aggression; breast; sexual activity; organoleptic; livestock; cell growth; analignant; prostate; ovarian; oncofoetal; hyperplastic; pregnancy; endometriosis;
                Gaps
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                  0; Indels
Pred. No. 1.4e+06;
                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 30; 41pp; English.
                                                                                                                                                                                               AAW94891 standard; peptide; 9 AA.
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  100.0%;
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Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                           (first entry)
                      Conservative
                                                                                                                                                                                                                                                                                                               LHRH peptide fragment
                                                                                                                                                                                                                                                                                                                                                                                                                prostate; ovarian; on
inflammatory response
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                                                          2 HWSYGLRP 9
                                                                                                 HWSYGLRP 9
  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                           11-MAY-1999
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                      Matches
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The present sequence is a peptide fragment of human luteinising hormone releasing hormone (also known as LHRH, GrRH and gonadotrophin releasing hormone). It was used to demonstrate the novel adjuvant of the invention, which has lower reactogenicity then previous compositions. Vaccination of humans and animals against LHRH can be used as a method of fertility control, as well as enabling the control and treatment of disorders of the reproductive organs, such as testicular, breast, prostate enlargement and endometriosis. The composition of the invention contains an anionic macromolecule and a saponin component, the latter of which his an immunostimulant, and it can also be used with other immunogens including soluble protein antigens, peptide haptens conjugated to a carrier protein and whole viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adjuvant composition for manufacturing an immunogenic composition that can elicit an immune response in an animal, comprises an ionic polysaccharide component and a saponin component that is an immunostimulating complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                         Human, LHRH; GnRH; luteinising hormone releasing hormone; gonadotrophin releasing hormone; fertility control; cancer; endometriosis; prostate enlargement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.3%; Score 52; DB 3; Length 9; 100.0%; Pred. No. 1.4e+06; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 50; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB08104 standard; peptide; 9 AA.
                                                                                                       AAB15363 standard; peptide; 9 AA.
                                                                                                                                                                                                Human LHRH peptide SEQ ID NO: 2.
                                                                                                                                                                                                                                                                                                                                                                                      99WO-AU001167.
                                                                                                                                                                                                                                                                                                                                                                                                                   99AU-00008073.
                                                                                                                                                                      (first entry)
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nes 8; Conserv
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HWSYGLRP
                            HWSYGLRP
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                                                                                                                                                                                                                                                                                                Homo sapiens
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Matches
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ID AABC
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AC AABC
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Gaps

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Sequence 9 AA;
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29-NOV-1991
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                                                                                                                                                                                                                            RESULT 3
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activities. (I) can be used as GnRH agonists used in combination with selective osstrogen receptor modulators, selective androgen receptor modulators, selective androgen receptor modulators, sex hormone synthesis inhibitors, lyase inhibitors, receptor type tyrosine kinase inhibitors, bone metabolism regulators, receptor mimunocherapy drugs, cytokine/chemokine inhibitors or endothelin receptor antagonists for treating and preventing endometriosis, myometrium tumour, Alzheimer's disease, circulatory system disorders, mnopausal disorders, irregular periods, cancer metastasis, premenstrual syndrome, muscular prostatomegally or prostate cancer or breast cancer or their reoccurrence or metastasis. Combination enhances the quality of life by enhancing GnRH agonist activity and/or reducing side effects. The present sequence increases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Distance adenocarcinoma, benign hypertrophy of the prostate,
                                                                                                                                                                                                                                                                                                                                                                                                                LHRH; Follicle Stimulating Factor; FSH; acne; hirsutism; dysmenorrhea; processes puberty; endometriosis; prostate cancer; tengenty prostate hypertrophy; mammary tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Pro-NH-(CH2)n-CH3 (n=0-2), Pro-NH-(CH2)2-OH or protected by pyrrolidino or morpholino gp."
                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                      Indels
                                                                                                                                                                                96.3%; Score 52; DB 6; Length 8; 100.0%; Pred. No. 1.4e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Luteinising Hormone Releasing Hormone analogue #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= OTHER
/note= "pyroglutamic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                 AAP10414 standard; protein; 9 AA.
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                                                                                                                                                                                          Similarity 100.8; Conservative
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(revised)
(revised)
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                                                                                                                                                                                                                          HWSYGLRP 9
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                                                                                                                                                             Sequence 8 AA;
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10-MAR-2003
01-JUL-2002
17.DEC-1992
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                                                                                                                                        invention
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A composition is claimed containing LHRH or its analogues. The composition is used to treat prostate adenocarcinoma, benign hypertrophy of the prostate, endometriosis, dysmenorrhea, hirsutism, hormone-dependent mammary tumours, for treatment or prevention of precocious puberty, delaying the onset of puberty and for treating acne. The compositions may also contain antiandrogens. See AAP10411-P10418 (Updated on 01-UUL-2002 to add missing PI field.) (Updated on 10-WMR-2003 to add missing os field.) (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsn. contg. gonadoliberin or its analogues - for treating parathormone deficiency states, e.g. hypocalcaemic conditions or hypertension.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The inventors claim a composn. for treating metabolic disorders caused by inadequete secretion of endogenous parathormone (PTH) which contains, apart from an acceptable carrier, gonadoliberin or agonists at least as strongly active as gonadoliberin. For parenteral use these provide 0.5-5 micrograms gonadoliberin per unit dose, and for application to mucosa (incranasally) 10-200 micrograms per dose, for an adult of average wt. (Updated on 03-0CT-2002 to add missing 0S field.)
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP50568 standard; protein; 9 AA.
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(first entry)
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Best Local Similarity 100.
Matches 8, Conservative
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Modified-site
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Length 9;

DB 1;

Score 52;

96.3%;

Query Match

Page 15; 27pp; French

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2004, 08:58:48; Search time 15.0584 Seconds Run on:

(without alignments) 187.635 Million cell updates/sec

US-09-848-834A-1 54 Title: Perfect score:

1 XHWSYGLRPX 10 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* geneseqp1980s:* Database :

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abp96550 Gonadot	Aap10414 Luteinisi	89	1881	Aab15363 Human LHR	Aab08104 Amino aci	Aab90979 Luteinisi	Aab90972 Luteinisi	Aab59836 GnRH pept	Aao16785 Sustained	Aae29840 Gonadotro	Abp96021 Gonadotro	Aap10416 Luteinisi	Aapl0411 Luceinisi	Aap10097 Sequence	7	Aap50222 Gonadotro	Aap60127 Gonadolib	103	Aap60576 Novel dec	Aap70922 Luteinisi	Aap90630 Sequence	5713	6819	Aar33434 Therapeut
ID	66	AAP10414	AAP50568	AAW94891	AAB15363	AAB08104	AAB90979	AAB90972	AAB59836	AA016785	AAE29840	ABP96021	AAP10416	AAP10411	AAP10097	AAP20277	AAP50222	AAP60127	AAP61403	AAP60576	AAP70922	AAP90630	AAR15713	AAR26819	AAR33434
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Aar62689 LHRH hapt Aar31197 LHRH pept Aar75152 Gonadotro Aar66845 Gonadotro	0.0040		2541 265 265 265	Aay03864 Amino aci Aay31180 Ubiquitin Aay31176 Ubiquitin
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ALIGNMENTS

ABP96550 standard; peptide; 8 AA. ABP96550

ABP96550;

(first entry) 27-MAY-2003

Gonadotrophin releasing hormone agonist gonadrelin peptide.

Gonadotrophin releasing hormone agonist; GnRH agonist; combination drug; pharamacutical; breast cancer; endometricals; myometrium tumour; Alzheimer's disease; circulatory system disorder; menopausal disorder; irregular period; cancer metastasis; premenstrual syndrome; osteopathy; muscullar distress; calcium/phosphorus imbalance; SBRM; synaecological; selective oestrogen receptor modulator; cytostatic; nootropic; muscular; neuroprotective; cardiovascular; endocrine; osteopathic; prostatomegally; prostate cancer.

Synthetic.

WO2003015820-A1.

27-FEB-2003.

08-AUG-2002; 2002WO-JP008130.

10-AUG-2001; 2001JP-00244616.

(TAKE) TAKEDA CHEM IND LTD.

Furuya S, Kusaka M;

WPI; 2003-300573/29.

Pharmaceutical composition e.g. for breast cancer comprises gonadotrophin releasing hormone agonist and selective estrogen receptor modulator.

Disclosure; Page 9; 73pp; Japanese.

The present invention describes a pharmaceutical composition (I) for treating breast cancer, endometricass, myometrium tumour, Alzheimer's disease, circulatory system disorders, menopausal disorders, irregular periods, cancer metastesis, premenstrual syndrome, muscular distress or osteopathies due to calcium/phosphorus imbalance. (I) comprises a gonadotrophin releasing hormone (GnRH) agonist and a selective ostrogen receptor modulator (SERM). (I) has cytostatic, gynaecological, nootropic, neuroprotective, cardiovascular, endocrine, muscular and osteopathic

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R. EMBL; AY204708; AAP06795.1; C.extracellular; IEA.

R. GO; GO:000576; C.extracellular; IEA.

R. GO; GO:0005775; P:development; IEA.

R. ThterPro: IPRO0122; GRRH.

R. PROSITE; PS004473; GNRH; 1.
Gaps
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01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Preprogonadotropin-releasing hormone 2 precursor.
Cinda intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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74.1%; Score 40; DB 5; Length 165;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels
2; Indels
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0; Mismatches
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6; Conservative
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                                                                                            66 HWSYALSP 73
                                           2 HWSYGLRP 9
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Matches
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Q86D88
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Search completed: March 10, 2004, 09:25:19 Job time: 11.8833 secs

67 HWSYALSP 74

2 HWSYGLRP 9

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Query Match
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01-JUN-2003 (
01-JUN-2003 (
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STRAIN=NCC 2705;
MRDLINE=22299977; PubMed=12381787;
Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
Pridmore R.D., Arigoni F.;
"The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
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01-0CT-2002 (TrEWBLrel. 22, Last sequence update)
01-0CT-2003 (TrEWBLrel. 24, Last annotation update)
00-dundotropin-releasing hormone.
Alosa sapidissima (American shad).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei; Clupeomorpha, Clupeidae,
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Bacteria, Actinobacteria, Actinobacteridae, Bifidobacteriales,
Bifidobacteriaceae, Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abraham E., Golhilf Y., Zohar Y.;

"American shad (Alosa sapidissina) hrGnRH sequence.";

"Lamerican shad (Alosa sapidissina) hrGnRH sequence.";

"Submitted (Aug-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AF536381; AAN04492.1; -.

GO; GO:0005179; Phormone activity; IEA.

GO; GO:0001279; Phormone activity; IEA.

GO; GO:0001279; Phormone activity; IEA.

InterPro; IPR022012; GnRH.

PERM; PROSITE; PS00446; GRH.

PROSITE; PS004473; GNRH; 1.

PROSITE; PS00473; GNRH; 1.
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                                                                                                                                DB 13; Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                             Indels
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AY320285, AAP84607.1, -. NON TER 1
                                                                                 SEQUENCE 72 AA; 8064 MW; 0FAACA4E2AB792BF CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Carbamoyl-phosphate synthase large chain.
CARB OR BL0068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1127 AA.
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Pred. No. 2.3;
1; Mismatches
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75.0%;
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Best Local Similarity 75...
6; Conservative
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NCBI_TaxID=34773;
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Q8G815;
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QBJH60
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MEDIUNE=2589575; PubMed=12697698;

A MEDLINE=2589575; PubMed=12697698;

Adams B.A., Tello J.A., Erchegyi J., Warby C., Hong D.J.,

Adams B.A., Tello J.A., Erchegyi J., Warby C., Hong D.J.,

Akinsanya K.O., Mackie G.O., Vale W., Rivier J.E., Sherwood N.M.;

"Six Novel Gonadorropin-Releasing Hormones Are Encoded as Triplets on

"Six Novel Gonadorropin-Releasing Hormones Are Encoded as Triplets on

"Six Novel Gonadorropin-Releasing Hormones Are Encoded as Triplets on

Encodering In Processor In Proceeding Inc.";

Embl. AN204709; AAP06796-1; --

R GO, GO:000570; C:extracellular; IEA.

R GO; GO:0007275; P:development; IEA.

R GO; GO:0007275; P:development; IEA.

R Fam; PF00446; GRRH; 1.

R PROSITE; PS00473; GNRH; 3.
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Warayota: Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
NCBI_TaxID=7719;
RMBL; AGUAGASI; AGUAGASI; I. R. RGO; GO: 0005524; F:ATP binding; IEA.

GO; GO: 0005524; F:ATP binding; IEA.

GO; GO: 0004666; F:ATP binding; IEA.

GO; GO: 0006524; F:ATP binding; IEA.

GO; GO: 0006526; P:arginine biosynthesis; IEA.

GO; GO: 0006526; P:arginine biosynthesis; IEA.

GO; GO: 0006526; P:arginine biosynthesis; IEA.

GO; GO: 0019856; P:primidine base biosynthesis; IEA.

IN INCEPPO; IPR005439; CPASE_LD:

R INCEPPO; IPR005448; CPASE_LD:

R INCEPPO; IPR005489; CPASE_LD:

R INCEPPO; IPR005489; CPASE_LD:

R PÉTAN; PR00248; CPASE_LD:

R PROSTITE; PR00098; CPASE_LD:

R PROSTITE; 
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gonadctropin-releasing hormone 7.
gonadctropin-releasing hormone 8.
gonadctropin-releasing hormone 4.
GnRH-associated peptide.
GnRH-associated peptide.
W; C2962E474F4163C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Preprogonadotropin-releasing hormone 2 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 16; Length 1127;
Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40; DB 5;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19119 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.9%;
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
74
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100
133
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32

HWSYGLSP

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Q805A5

RESULT 8

0805A5

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STRAIN=1021;
MEDLINE=21396509; PubMed=11481432;
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barnoy-Hubier F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Kaaring D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
"Nucleotide sequence and predicted functions of the entire
Sinorhizobhum mellioti pSymA megaplasmid.";
Broc. Natl. Acad. Sci. U.S.A. 98:3883-9888(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain; duludur L.A., Somoza G.M.; bullqur L.G., Miranda L.A., Somoza G.M.; constructive of three GnRH cDNA sequences in the pejerrey fish odonteethes bonariensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-007-2003 (TrEMBLrel. 25, Created)
01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Gonadotropin-releasing hormone (Fragment).
Odontesthes bonariensis.
Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Atherinoidei; Atherinidae; Atherinopsinae;
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                                                                                                                                                                                                                                                                                                                                                                     Plasmid DSymA (megaplasmid 1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiacea; Sinorhizobium/Ensifer group; Sinorhizobium.
NCBI_TAXID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 374; 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                             vi-uun-2003 (TrEMBirel, 24, Last annotation update) Putative muconate cycloisomerase (EC 5.5.1.1).
RA0797 OR SMA1461.
Anizobium mellioti (Sinorhizobium mellioti).
                                                                                                                                                                                                                                      Last sequence update)
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                                                                                                                          374 AA.
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85.7%; Pred. No. 9.4;
ive 1; Mismatches
                                                                                                                                                                                                   Created)
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                                                                                                                              PRT;
                                                                                                                                                                                                (TrEMBLrel. 19, (TrEMBLrel. 19, 1) (TrEMBLrel. 24, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR, E95361; E95361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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01-DEC-2001
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                                                                                                                              092YR6
                                                             RESULT 10
Q92YR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                         SOW WHEN THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parhar I.S., Ogawa S., Sakuma Y.;
"Molecular cloning of tilapia (oreochromis niloticus) GnRH cDNA.";
Submitted (FBB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AB101665; BAC56849.1; -GO, GO: 0005576; C: extracellular; IEA.
GO; GO: 0005183; F:luteinizing hormone-releasing factor activity; IEA.
GO; GO: 0007275; P:luteinizing hormone-releasing factor activity; IEA.
InterPro; IPR004071; GnRH; IEA.
InterPro; IPR004079; Gonadoliberini.
PRINTS; PR01541; GONADOLIBRNI.
PRINTS; PR01541; GONADOLIBRNI.
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Micropogonias undulatus (Atlantic croaker).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Perciformes, Percoidei,
Sciaenidae; Micropogonias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                              Q805A5;
01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 25, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Seabream-type gonadotropin-releasing hormone precursor.
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Labroidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
SEABREAM-TYPE GONADOTROPIN-RELEASING
HORMONE.
2417F7737DBC97E3 CRC64;
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Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 13; Length 98;
Pred. No. 0.6;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hormone precursor.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY324668; AAQ16501.1; -.
SEQUENCE 120 AA; 13236 MW; 33334470D2E35492 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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86
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PRT;
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llarity 87.5%;
Conservative 0
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Best Local Similarity 87.5°
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                             Cichlidae, Oreochromis.
NCBL_TaxID=8128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 HWSYGLSP 31
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Matches 7; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
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us-09-848-834a-1.open.rspt

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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
60-JUN-2003 (TrEMBLrel. 24, Last annotation update)
60-JUN-2003 (TrEMBLrel)
60-JUN-2003 (Gonadoliberin)
60-JUN-2003 (Go
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GONADOTROPIN-RELEASING HORMONE ASSOCIATED PEPTIDE.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005183; F:luteinizing hormone-releasing factor activity; IEA.
GO; GO:0007575; F:luteinizing hormone-releasing factor activity; IEA.
GO; GO:000775; F:luteinizing hormone-releasing factor activity; IEA.
InterPro; IPR004079; GonadoliberinI.
PRINTS; PR01541; GONADOLIBRNI.
PROSITE; PS00473; GNRADOLIBRNI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEABREAM-TYPE GONADOTROPIN-RELEASING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 13; Length 96;
Pred. No. 0.58;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 46; DB 13; Length
Pred. No. 0.57;
0; Mismatches 1; Indel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FA3202565EA00DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           GONADOTROPIN-RELEASING HC
GNRH-ASSOCIATED PEPTIDE.
E57DBA832FC078D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
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PROSITE; PS00473; GNRH; 1.
Amidation; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                             1 22 Pr
23 32 Gv
36 94 GJ
94 AA; 10396 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 AA; 10560 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 HWSYGLSP 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 HWSYGLSP 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004079;
Pfam; PF00446; GnRH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 HWSYGLRP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HWSYGLRP 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS(Amidation; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amano M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                            Signal.
SIGNAL
CHAIN
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha; Perciformes, Labroidei,
Cichlidae, Orecohromis.
                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update).
01-MAY-1999 (TrEMBLrel. 10, Last annotation update).
01-MAY-1999 (TrEMBLrel. 24, Last annotate).
01-MAY-1999 (TrEMBLrel. 24, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTM-2003 (TrEMBLrel. 24, Last annotation update)
GORHI preprohormone precursor (Seabream-type gonadotropin-releasing hormone precursor).
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Farahmand H., Rahman M.A., Sohm F., Hwang G.-L., Maclean N.;

"Isolation and Expression of Tilapia (Oreochromis niloticus) Serine

"Type GnRH Coding and Requilatory Sequences.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Sato H., Sakuma Y. Parhar I.S.;
Sato H., Sakuma Y. of three Kinds of GRRH genes and S' untranslated regions in tilapia (Oreochromis miloticus).";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AF467291; AAM90220.1; -..
EMBL; AB104861; BAC65154.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 AA; 9871 MW; 0D2463533D96782A CRC64;
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Best Local Similarity 87.5
7, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 HWSYGLRP 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sparidae, Sparus.
NCBI_TaxID=8175;
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fishes."; Carcollour the EMBL/GenBank/DDBJ databases.
Lishdad (Aug-2002) to the EMBL/GenBank/DDBJ databases.
Resublitated (Aug-2002) to the EMBL/GenBank (Aug-2006) to the EMBL/Gengling factor activity; IEA.
Resublitated (Aug-2006) to the EMBL/Gengling factor
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.

BMBJ; AB089312; BAC07228.1; -.

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0007275; P:development; IEA.

InterPro; IPR0402012; GnRH.
InterPro; IPR04405; GonadoliberinI.

PRINTS; PR01541; GONADOLIBRNI.

PROSITE; PS00473; GNRH; 1.
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01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-077-2002 (TrEMBLrel. 24, Last annotation update)
01-0707-2003 (TrEMBLrel. 24, Last annotation update)
Gonadotropin-releasing hormone (Fragment)
Acanthopagrus latus (Yellowfin porgy).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Sparidoe; Acanthoperrygii; Percomorpha; Perciformes; Percoidei;
NCBL_TAXID=8177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kato M., Elmesiry G.E.;
"Sequence comparison of GnRH genes in closely-related Sparidae
                                                          Kato M., Elmesiry G.E.; "Sequence comparison of GnRH genes in closely-related Sparidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 13; Length 68;
Pred. No. 0.4;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 13; Length 64;
Fred. No. 0.37;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 AA.
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Best Local Similarity 8/.-
7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 HWSYGLSP 23
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SEQUENCE FROM N.A.
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[1]
SEQUENCE FROM N.A.
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SEQUENCE
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OBJIF4;
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EMBL; AB089313; BAC07229.1; --
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005183; F:luteinizing hormone-releasing factor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR002012; GnRH.
InterPro; IPR004049; GonadoliberinI.
PFam; PF00446; GnRH; 1.
PROMITS; PR01541; GONADOLIBRNI.
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08JIF2;
01-OCT-2012 (TEMBLE-1 . 22, Created)
01-OCT-2002 (TEMBLE-1 . 22, Last sequence update)
01-UN-2003 (TEMBLE-1 . 24, Last annotation update)
01-UN-2003 (TEMBLE-1 . 24, Last annotation update)
Gonadorropin-releasing hormone (Fragment).
Pagrus major (Red aca bream) (Chrysophrys major).
Enkaryota; Metazoa; Chrodata, Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Perconfeti; Perc
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                                                                                                                                                                                                                                                                                       96.3%; Score 52; DB 13; Length 91; 100.0%; Pred. No. 0.043; tive 0; Mismatches 0; Indels
                                                                                                                                               MGNRH.
GNRH ASSOCIATED PEPTIDE.
BA15C9DC08434A7B CRC64;
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01-0cr-2002 (TrEMBLrel. 22, Last sequence update)
01-0th-2003 (TrEMBLrel. 24, Last annotation update)
Gonadotropin-releasing hormone (Fragment).
Dentex dentex.
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   PRINTS; PRO1541; GONADOLIBRNI.
PROSTITE; PSO0473; GNRH; 1.
Amidation; Hormone; Signal.
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33 91
91 AA; 9893 MW;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 8; Conservative
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NCBI_TaxID=143350;
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Chubo K., Suetake H., Aida K.;

"A splicing variant for the prepro-mammalian gonadotropin-releasing
thermone (prepro-mgnaH) mkNa is present in the brain and various

"A splicing variant and various

"I col. Sci. 16:645-651(1999).

"I col. Sci. 16:645-651(1999).

"I col. Sci. 16:645-651(1999).

"I shill LARITY).

"I SIMILARITY)

"I SELONGS TO THE GNRH FAMILY.

EMBL; AB02699; BAA83608.1, -

"OR GO:0005975; C:extracellular; IEA.

GO; GO:0005975; C:extracellular; IEA.

GO; GO:0007275; P:development; IEA.

RO; GO:0007275; P:development; IEA.

InterPro; IPR0046079; Gonadoliberini.

Pfam; PF00446; GRRH; 1.
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TISSUE=Brain;
Okubo K., Suetake H., Aida K.;
Expression of two gonadotropin-releasing hormone (GnRH) precursor genes in various tissues of the Japanese eel and evolution of GnRH.";
Zool. Sci. 16:471-478 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ol-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 24, Last annotation update)
01-MAY-2000 (TrEMBLrel. 24, Last annotation update)
Prepro-MGRH precursor (Gonadoliberin) (Gonadotropin-releasing hormone) (LH-RH) (Luliberin).
Anguilla japonica (Japanese eel).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
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Q77666
Q970714
Q9W714
Q99E34
Q90E32
Q90E32
Q91E8P
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Q90EBP
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                                         Anguilla.
NCBI_TaxID=7937;
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Search completed: March 10, 2004, 10:25:47 Job time : 8.85992 secs
                        Query Match
Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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US-10-117-364-1
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TITLE OF INVENTION: LHRH Antagonist Peptides

FILE REFERENCE: PPI-007CPUS
CURRENT APPLICATION WURBER: US/10/115,553

CURRENT FILING DATE: 2002-04-02

PRIOR APPLICATION WURBER: EARLIER APPLICATION NUMBER: 08/973,378

PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-06

PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 1.00

SOFTWARE: PATENTING DATE: 1995-06-07
                                                                                                                                                                                                                                                   Query Match 96.3%; Score 52; DB 13; Length 10; Best Local Similarity 100.0%; Pred. No. 0.022; Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 14; Length 10;
Pred. No. 0.022;
0; Mismatches 0; Indels
               OTHER INFORMATION: synthetic FEATURE:
NAMES (CATION: (1)...(1)
LOCATION: (1)...(1)
OTHER INFORMATION: Glu is modified with a pyro group. FEATURE:
                                                                                                                                          NAME/KEY: misc_feature

: LOCATION: (10)...(10)

: OTHER INFORMATION: Gly is modified with -NH2 group.

US-10-184-126-1
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Publication No. US20030044936A1
Fublication No. US20030044936A1
FUBERRAL INFORMATION:
APPLICANT: Hwang, Jaulang
APPLICANT: Hau, Chia-Tse
APPLICANT: Ting, Chun-Jen
TITLE OF INVENTION: PEPTIDE REPEAT INMUNOGENS
FILE REPRENCE: 08919-071001
CURRENT APPLICATION NUMBER: US/10/122,483
CURRENT APPLICATION NUMBER: 09/412,558
FRIOR PILING DATE: 1999-10-05
FRIOR PILING DATE: 1999-10-05
NUMBER OF SEQ ID NOS: 13
SOPTWARE: PastSEQ for Windows Version 4.0
LENGTH: 10
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Publication No. US20030040482A1
GENERAL INFORMATION:
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100.0%;
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Best Local Similarity 100.
Matches 8; Conservative
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US-10-115-553-1
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CRGANISM: Homo sapiens
US-10-122-483-1
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Sequence 1, Application US/10117364

Publication No. US20030181385A1

GENERAL INFORMATION:

TITLE OF INVENTION: LHRH Attagomist Peptides

TITLE OF INVENTION: LHRH Attagomist Peptides

CURRENT FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/08/973,378

PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-06

PRIOR PELICATION NUMBER: EARLIER APPLICATION NUMBER: 08/480,494

PRIOR FILING DATE: EARLIER FILING DATE: 1995-06-07

SOPTHARE: PATCHING DATE: EARLIER FILING DATE: 1995-06-07

SOPTHARE: PATCHING DATE: 2.0
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DB 14; Length 10; 0.022;
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Pred. No. 0.022;
0; Mismatches 0; Indels
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Score 52; DB
Pred. No. 0.0
0; Mismatches
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Best Local Similarity 100.0%; Pr
Matches 8; Conservative 0;
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InterPro; IPR002012; GGRH.

InterPro; IPR004019; GGRH.

Pfam; PF00446; GRH; 1.

PRINTS; PRO1454; GONDOLIBRNI.

PROSITE; PS00473; GONDOLIBRNI.

Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus; Signal; Multigene family; Pyrrolidone carboxylic acid.

23 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROGENIAL I.

GONADOLIBERIN I.

GONRADOLIBERIN I.

GNRH-ASSOCIATED PEPTIDE I (POTENTIAL).

PYRROLIDONE CAMBOXYLIC ACID (BY
SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).

(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                              Okuzawa K., Granneman J., Bogerd J., Goos H., Zohar Y., Kagawa H.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: Stimulates the secretion of gonadotropins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                      similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the GnRH family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 AA; 10566 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; D86582; BAA13129.1; -.
NCBI_TaxID=143350;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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    NATURAL SERVICE COCCOCCOCCE SERVICE SE
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Search completed: March 10, 2004, 09:13:45 Job time : 2.82879 secs

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SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                            MEDITNE=99061809; PubMed=9845669; Chow M.M., Kight K.E., Gochilf Y., Alok D., Stubblefield J., Zohar Y.; Chow M.M., Kight K.E., Gochilf Y., Alok D., Stubblefield J., Zohar Y.; Multiple GRRHs present in a teleost species are encoded by separate genes: analysis of the sbGnRH and cGnRH-II genes from the striped bass, Morone saxatilis."; J. Mol. andocrinol. 21:277-289(1998).
i. PUNCIION: Stimulates the secretion of gonadotropins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; LPKOURO, D. PERO, PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Gonadoliberin I precursor (Gonadotropin-releasing hormone I) (GnRH-I)
(LH-RH I) (Luliberin I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pagrus major (Red sea bream) (Chrysophrys major).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleosta; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Sparidae; Pagrus.
28-FEB-2003 (Rel. 41, Last annotation update)
Gonadoliberin I precursor (Gonadotropin-releasing hormone I) (GnRH-I)
(LH-RH I) (Luliberin I).
                                                                                                                             Morone saxatilis (Striped bass).
Morone saxatilis (Striped bass).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AMIDATION (G-33 PROVIDE AMIDE GROUP) (BY SIMILARITY).
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GNRH-ASSOCIATED PEPTIDE I (P
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 95;
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Pred. No. 0.069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the GnRH family.
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InterPro; IPR002012; GnRH.
InterPro; IPR004079; GonadoliberinI.
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Moronidae; Morone
NCBI_TaxID=34816;
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PEPTIDE
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ID GON1_P
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                                                                                                                  GNRH1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatice and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its mode by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01541; GONADOLIBRNI.
PROSITE; PS00473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus; Signal; Multigene family; Pyrrolidone carboxylic acid.
1 22 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U31865; AAC59691.1; -.

EMBL; AF076961; AAC27716.1; -.

PIN; I50739; I50739; IS0739; G. extracellular; NAS.

GO; GO:0005576; C. extracellular; NAS.

GO; GO:0005183; F:luteinizing hormone-releasing factor activity; NAS.

GO; GO:0007575; Pedvelopment; IDA.

InterPro; IPR002012; GRH.

InterPro; IPR004079; GonadoliberinI.
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GNRH-ASSOCIATED PEPTIDE I (POTENTIAL).
PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-33 PROVIDE AMIDE GROUP).
ENGHTPEKK -> KMDYGHSRERFL (IN REF. 1).
ES7DBA8333278D7 CRC64;
                                            SEQUENCE FROM N.A.
MEDLINE=99061142; PubMed=9843638;
Mhite R.B., Fernand R.D.;
Mhite R.B., Fernand R.D.;
"Ontogeny of gonadctropin-releasing hormone (GnRH) gene expression reveals a distinct origin for GnRH-containing neurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 94;
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Pred. No. 0.068;
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                                                                                                                                                                                                                                                                                                                              23-32, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                           Gen. Comp. Endocrinol. 112:322-329(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10382 MW;
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Pfam; PF00446; GnRH; 1
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Best Local Similarity
Matches 7; Conserv
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16-OCT-2001
16-OCT-2001
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Gaps

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(Rel. 40, Created) (Rel. 40, Last sequence update)

RESULT 14 GON1 MORSA GON1

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CONFLICT

MOD_RES PEPTIDE

(POTENTIAL)

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HWSYGLOP 32
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PEPTIDE
PEPTIDE
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GON1_HAPBU
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Matches
                     SOLUTION SERVICE SERVI
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                                                                                                                                                                                                                                              MEDINE-1135238; PubMed-1882082;
Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
"Primary structure of two forms of gonadotropin-releasing hormone from brains of the American alligator (Alligator mississippiensis).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
         (GnRH-I) (LH-RH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB=Hypothalamus;
King J.A., Millar R.P.;
"Structure of avian hypothalamic gonadotrophin-releasing hormone.";
S. Afr. J. Sci. 78:124-125(1982).
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GONI CHICK
GONI CHICK
GONI CHICK
F37042; P20407;
01-FEB-1991 (Rel. 17, Created)
01-UUN-1994 (Rel. 29, Last sequence update)
01-UUN-1994 (Rel. 29, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
(Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing)
(Luteinizing hormone-releasing hormone I) (Granadotropin-releasing)
(Luteinizing hormone-releasing hormone I) (Granadotropin-releasing)
(Luteinizing hormone-releasing)
                              (Luliberin I).

Alligator mississippiensis (American alligator).

Eukaryota, Metazoa, Chordata; Craniata; Vertebrata, Euteleostomi;

Archosauria, Crocodylidae, Alligatorinae, Alligator.
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MEDLINE=8256778; PubMed=7050119;
King J.A., Millar R.P.;
King J.A., Millar R.P.;
"Structure of chicken hypothalamic luteinizing hormone-releasing hormone. II. Isolation and characterization.";
J. Biol. Chem. 257:10729-10732(1982).
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MEDLINE=94059355; PubMed=7902095;
Dunn I.C., Chen Y., Hook C., Sharp P.J., Sang H.M.;
"Characterization of the chicken preprogonadotrophin-releasing
                                                                                                                                                                                                                                                                                                                                                                          F from brains or the American be a regul. Pept. 33:105-115(1991).

C -1- FUNCTION: Stimulates the secretion of gonadotropins.

C -1- SUBCELLULAR LOCATION: Secreted.

C -1- SUBCILLULAR LOCATION: Secreted.

PIR, A60066; RHAQ1.

R PIR, A60066; RHAQ1.

R PÉBM: PF00446; GnRH: 1.

R PGAM: PF00446; GnRH: 1.

R POSTIE; PS00473; GNRH: 1.

WHOTHOME: Amidation; Hypothalamus; Pyrrolidone carboxylic acid by Hypothalamus; Pyrrolidone Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
Gonadoliberin I (Gonadotropin-releasing hormone I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 1;
Pred. No. 0.003;
; Mismatches (
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Mol. Endocrinol. 11:19-29(1993)
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Local Similarity 87.5%;
les 7; Conservative
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                                                                                                                                                                   [1]
SEQUENCE.
`~™R≃B.
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GON1 CHICK
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PIR; I50644; I50644.

QO; GO:0005518; Filuteinizing hormone-releasing factor activity; IDA.
GO; GO:0007218; Filuteinizing hormone-releasing factor activity; IDA.
InterPro; IPR002012; GARH.
InterPro; IPR004079; GARH.
InterPro; IPR004079; GARH.
PRINTS; PR00446; GARH; PR0040618; PR00406; GARH; PR00406; GARH; ICACONDOLIBRNI.
PROSITE; PS00473; GNRADOLIBRNI.
Cleavege on pair of basic residues; Hormone; Amidation; Hypothalamus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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01-0CT-1996 (Rel. 34, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Progonadoliberin I precureor [Contains: Gonadoliberin I (Luteinizing hormone releasing hormone I) (Gonadotropin-releasing hormone I) (GNRH-1) (LH-RH I) (Luliberin I); GRRH-associated peptide I].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haplochromis burtoni (Burton's mouthbrooder).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
Cichlidae; Astatotilapia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95396797; PubMed=7667296; White S.A., Kasten T.L., Bond C.T., Adelman J.P., Fernald R.D.; Three gonadotropin-releasing hormone genes in one organism suggest novel roles for an ancient peptide."; Proc. Natl. Acad. Sci. U.S.A. 92:8363-8367 (1995).
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[4]

MEDLINE-82265777; PubMed=7050118;

King J.A., Millar R.P.;

King J.A., Millar R.P.;

King J.A., Millar R.P.;

King J.A., Millar R.P.;

Miscretive of chicken hypothalamic luteinizing hormone-releasing hormone. I. Structural determination on partially purified material., S. Eto., Chem. 257:10728 (1982).

J. Biol., Chem. 257:10722-10728 (1982).

J. FUNCTION: Stimulaes the secretion of gonadotropins.

SUBCELLULAR LOCATION: Secreted.

SIMILARITY: Belongs to the GRRH family.
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GNRH-ASSOCIATED PEPTIDE I.
PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 1; Length 92;
Pred. No. 0.028;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 AA.
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nes 7; Conservative
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the GRBH family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00446; vara, 4.
PRINTS; PR01541; GONADOLIBRNI.
PROSTTE; PS00473; GNRH, 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Signal; Pyrrolidone carboxylic acid.
The control of the carboxylic acid.
The carboxylic acid.
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APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
27-Septonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I) (Luteinizing hormone releasing hormone releasing hormone I) (Gonadotropin-releasing hormone I) (GORH I) (Luliberin I); GNRH-associated peptide I).
                                                                                                                                                                                                                                                                                           Būkaryota, Metazoā, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Scandentia, Tupaiidae, Tupaia.
                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Hypothalamus;
MEDLINE=97079639; PubMed=8921350;
Kasten T.L., White S.A., Norton T.T., Bond C.T., Adelman J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID (BY
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01-PBE-1991 (Rel. 17, Created)
01-PBE-2901 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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      92 A.A.
                                                                                                                                                                                                                                                                     Tupaia glis belangeri (Common tree shrew).
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InterPro; IPR004079; GonadoliberinI.
      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U63326; AAB16837.1; -.
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nes 8; Conservative
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      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=37347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fernald R.D.;
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GON1 ALLMI
ID GON1 ALLMI
      GON1 TUPGB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 235:1514-1517(1987).
-!- FUNCTION: Stimulates the secretion of gonadotropins, it stimulates
the secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1541; GONADOLIBRNI.
PROSITE; PS00473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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PROLACTIN RELEASE-INHIBITING FACTOR I.
APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87149087; PubMed=3547652; Adelman J.P., Bond C.T., Douglass J., Herbert E.; Mermanian genes transcribed from opposite strands of the same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-34 PROVIDE AMIDE GROUP).
494B5CG4DA8A3EB3 CRC64;
[2]
SEQUENCE FROM N.A.
MEDLINE-89384661; PubMed-2476669;
BONG C.T., Hayflick J.S., Seeburg P.H., Adelman J.P.;
"The rar gonadotropin-releasing hormone: SH locus: structure and hypothalamic expression...";
hypothalamic expression...";
MOI. Endocrinol. 3:1257-1262 (1989).
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0
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MEDINES=23105480; PubMed=1468115;
MA4er C.C., Marchetti B., Leboeuf R.D., Blalock J.E.;

"Thymocytes express a mRNA that is identical to hypothalamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.3%; Score 52; DB 1; Length 92; 100.0%; Pred. No. 0.005; 0; Indels cive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Central nervous system.
-!- SIMILARITY: Belongs to the GARH family.
                                                                                                                                                                                                                                                                                                                                                                                   luteinizing hormone-releasing hormone mRNA.";
Cell. Mol. Neurobiol. 12:447-454(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, S50870; AAB24572.1; EMBL, M12579; AAA41263.1; EMBL, M1579; AAA41263.1; EMBL, M1579; AAA41264.1; EMBL, M15527; AAA42141.1; ALT_SEQ. EMBL, M15529; AAA42139.1; EMBL, M15529; AAA42139.1; IncerPro; RRHG, RRHG, IncerPro; RRHG, EMBL, M15529; AMBC, AMBC,
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33 33
92 AA; 10500 MW;
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nes 8; Conservative
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MIM; 152760; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H., "Isolation of the gene and hypothalamic cDNA for the common precursor of gonadotropin-releasing hormone and prolactin release-inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Macde2671939; MEDVINE-89386682; PubMed-2671939; MEDVINE-8936682; Adelman J.P., Seeburg P.H., HayLinck J.S., Adelman J.P., Seeburg P.H., HayLinck J.S., Adelman Gonadotropin-releasing "The complete nucleotide sequence of the human gonadotropin-releasing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted.
PHARMACEUTICAL: Available under the names Factrel (Ayerst Labs),
Lutrepulse or Lutrelef (Ferring Pharmaceuticals) and Relisorm
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MEDLINE=85012739; PubMed=6090951;
Seeburg P.H., Adelman J.P.;
"Characterization of CDNA for precursor of human luteinizing hormone releasing hormone.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99318093; PubMed=10391209; Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N. Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                      21-JUL-1986 (Rel. 01, Created)
01-APR-1988 (Rel. 07, Last sequence update)
01-APR-1988 (Rel. 07, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
Promone I) (GnRH I) (Luliberin I) (Gonadorropin-releasing
peptide I] (GnRH I) (Luliberin I) (Gonadorelin); GnRH-associated
GNRH1 OR GNRH OR LHRH.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Rutherra; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 24-33.
MEDLINE-83126573; PubMed-6760865;
Tan L., Rousseau P.;
"The chemical identity of the immunoreactive LHRH-like peptide blosynthesized in the human placenta.";
Bloshem. Blophys. Res. Commun. 109:1061-1071(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor in human and rat.";
Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
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                                                                                        85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hormone gene.";
Nucleic Acida Res. 17:6403-6403(1989)
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MEDLINE=86094338; Pubmed=2867548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          releasing hormone.";
Nature 311:666-668(1984).
                                                                                           STANDARD;
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                                                                                             HUMAN
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                                                  RESULT 8
GON1_HUMAN
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01-APR-1988 (Rel. 07, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
[Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GnRH I) [Luliberin I); Prolactin release-inhibiting factor
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MEDIATE=8604338; PubMed=2867548;
AGAINTB=8604338; MASON A.J., Hayflick J.S., Seeburg P.H.;
Adalman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
Isolation of the gene and hypothalamic cDNA for the common precursor of gonadorrophin-releasing hormone and prolactin release-inhibiting factor in human and rat "I P. Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MIM, 152760. -.

GO, GO:0005625; C:soluble fraction, TAS.

GO; GO:0005631; P:luteinizing hormone-releasing factor activity; TAS.

GO; GO:00005267; P:ceall-cell signaling; TAS.

GO; GO:0007275; P:development, TAS.

GO; GO:0000285; P:negative regulation of cell proliferation; TAS.

GO; GO:0000165; P:signal transduction; TAS.

InterPro; IPR002012; GDRA.

InterPro; IPR005012; GDRA.

InterPro; IPR004079; GonadoliberinI.
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AMIDATION (G-34 PROVIDE AMIDE GROUP).
W -> S (in dbSNP:6185).
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30A72221B076FA79 CRC64;
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Pred. No. 0.005;
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MEDLINE=72065776; PubMed=4942726; Mateur A.V.; Mateur A., Nair R.M.G., Schally A.V.; Arimura A., Nair R.M.G., Schally A.V.; Eynthesis of the porcine LH- and FSH-releasing hormone by the solid-phase method.";
(Luteinizing hormone-releasing hormone I) (Gonadotiberin I (LH-RH I) rormone I) (Gonadotropin-releasing hormone I) (Gonza (Luliberin I); GnRH-associated peptide I]. WRH-OR GNRH.
                                                                                                                                                                                                                                    MEDINE=72114303; PubMed=4946067; Matsuo H., Schally A.V.; Structure of the portione H. and FSH-releasing hormone. II. "Structure of the proposed structure by conventional sequential confirmation of the proposed structure by conventional sequential
                                                            Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Hypothalamus;
Weesne (D., Matteri R.L., Becker B.A.;
Submitted (MAY-1994) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                    analyses.";
Biochem. Biophys. Res. Commun. 44:459-463(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                      iochem. Biophys. Res. Commun. 45:822-827(1971).
      Progonadoliberin I precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNTHESIS OF GONADOLIBERIN.
                                                                                                                                                                                                                         SEQUENCE OF 24-33.
                                                                                                                 NCBI_TaxID=9823;
                                     hormone I)
                                                       GNRH1
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                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF188754; AAL05972.1; -
60, GO:0005576; C:extracellular; NAS.
GO:0005183; F:luteinizing hormone-releasing factor activity; NAS.
GO:0000183; F:luteinizing hormone-releasing factor activity; NAS.
GO:0000003; P:hormone mediated signaling; NAS.
InterPro: IPR002012; GRRH.
InterPro: IPR004019; GonadoliberinI.
Pfan; PF00446; GnRH; 1.
PRINTS; PR01541; GONADOLIBRNI.
PROSTE; PS00473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION (G-35 PROVIDE AMIDE GROUP) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
         10-OCT-2003 (Rel. 42, Last annotation update)
Progonadoliberin I precursor [Contains: Gonadoliberin I (LHRH I)
(Luteinizing hormone releasing hormone I) (Gonadotropin releasing
hormone I) (GRRH I) (Luliberin I); GRRH-associated peptide I (GAPI)].
                                                                                                                                                                                                                                         "Cloning and characterization of cDNAs encoding the GRRH1 and GRRH2 precursors from bullfrog (Rana catesbeiana)."; 
J. Exp. Zool. 289:190-201(2001).

    similarity).
    SUBCELLULAR LOCATION: Secreted.
    TISSUE SPECIPICITY: Forebrain.
    DEVELOPMENTAL STAGE: Expressed at significantly higher levels during post-breeding. Not expressed in pituitary.
    SIMILARITY: Belongs to the GRRH family.

                                                                                  Rana catesbeiana (Bull frog).
Bukaryota; Metazoa; Chordaca; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
0
                                                                                                                                                             SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE
                                                                                                                                                                                   TISSUE=Forebrain;
MEDLINE=21102951; PubMed=11170016;
WANG L., YOO M.S., Kang H.M., Im W.B., Choi H.S., Bogerd J.,
Kwon H.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNRH-ASSOCIATED PEPTIDE I (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 90;
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PROGONADOLIBERIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.3%; Score 52; DB 1; I
100.0%; Pred. No. 0.0049;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GONADOLIBERIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10291 MW;
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                             GNRH1 OR GNRH
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PEPTIDE
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MEDLINE=72117544; PubMede4946275;
Baba Y., Arimura A., Schally A.V.;
Baba Y., Arimura A., Schally A.V.;
"On the tryptophan residue in porcine LH and FSH-releasing hormone.";
Biochem Biophys. Rea Commun. 45:483-487(1971).
-;- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS, PRO1541; GONADOLIBRNI.
PROSITE; PS00473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Signal; Pyrrolidone carboxylic acid.
1 23
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APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
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AMIDATION (G-34 PROVIDE AMIDE
8340474F32DDAA99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; DB 1; Length >1,
Pred, No. 0.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROGONADOLIBERIN I.
                                                                                                                                                              -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the GnRH family.
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                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, 132864; AAA31066.1; -.
InterPro, IPR002012; GnRH.
InterPro, IPR004079; GonadoliberinI.
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PEPTIDE
PEPTIDE
ACT_SITE
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SEQUENCE
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HWSYGLRP 32

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Last sequence update)
Last annotation update)

Created)

(Rel. 34, (Rel. 34, 1)

GON1 PIG ID GON1 PIG AC P49921; DT 01-0CT-1996 (DT 28-FEB-2003 (

RESULT 7

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STANDARD;

26 HWSYGLRP 33

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2 HWSYGLRP

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RESULT 4
GON1_XENLA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDIJNE=87069928; PubMed=3024317;
MEDIJNE=87069928; PubMed=3024317;
MASON A.J., Hayflick D.S., Zoeller R.T., Young W.S. III,
Phillips H.S., Nikolics K., Seeburg P.H.;
"A deletion truncating the gonadotropin-releasing hormone gene is responsible for hypogonadism in the hpg mouse.";
Science 234:1366-1371(1986).
-!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating
                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
[Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GnRH I) (Luliberin I), Prolactin release-inhibiting factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:95789; Gnrh.
InterPro; IPR002012; GnRH.
InterPro; IPR004019; GonadoliberinI.
PRIMTS; PR01541; GONZHOITBRNI.
PRIMTS; PR01541; GONZHOITBRNI.
PROSTE; PS00473; GNRH; I.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Signal; Pyrrolidone carboxylic acid.
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PROLACTIN RELEASE-INHIBITING FACTOR I.
APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-32 PROVIDE AMIDE
1C0766FA4826E4D9 CRC64;
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Pred. No. 0.0049;
0; Mismatches 0; Indels
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(Rel. 42, Last sequence update)
                                                 90 AA.
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-!- SIMILARITY: Belongs to the GRRH family.
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100.0%; Pre
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                                                    STANDARD;
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GON1_RANCA
ID GON1_RANCA
AC Q90Y63;
DT 10-0CT-2003 (
DT. 10-0CT-2003 (
                                                                                                                                                                                                                                                                                                                  GNRH1 OR GNRH.
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8
                                                    GON1 MOUSE
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Matches
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                                                          SOLUTION OF THE STANK WERE AND DEPOSE OF THE 
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                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Gonadoliberin I precursor (Gonadotropin-releasing hormone I) (GnRH-I)
(LH-RH) (Luliberin I).
Sengus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
NCRT TANDACAIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1541; GONADOLIBRNI.
PROSITE; PSO0473; GNRH; 1.
Cleavage on pair to basic residues; Hormone; Amidation; Hypothalamus;
Signal; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                          Gaps
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PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-34 PROVIDE AMIDE GROUP)
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MEDLINE=94185563; PubMed=8137750;
Hayes W.P., Wray S., Battey J.F.;
"The frog gonadotropin-releasing hormone-I (GnRH-I) gene has mammalian-like expression pattern and conserved domains in GnRH-associated peptide, but brain onset is delayed until
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 52; DB 1; Length 89; 100.0%; Pred. No. 0.0048; ive 0; Mismatches 0; Indels
96.3%; Score 52; DB 1; Length 67; 100.0%; Pred. No. 0.0036; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                         89 A.A.
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PIR, 151423; 151423.
InterPro, 178002012; GRH.
InterPro, 178004079; GonadoliberinI.
Pfam; PP00446; GRRH; 1.
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Best Local Similarity 100.
Matches 8; Conservative
      Query Match
Best Local Similarity 100.
Matches 8, Conservative
                                                                                                                                                                                                                                                                                                                            STANDARD;
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Length 63;

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                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jansen H.T., Stevens P.J., Zeitler P., Lehman M.N.,
Submitted (MAR-1997) to the BMBL/GenBank/DDBJ databases.
-!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
the secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).
AMIDATION (G-11 PROVIDE AMIDE GROUP) (BY
                                                                                                                                            Gaps
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GNRH-ASSOCIATED PEPTIDE I.
APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY.
                                                       PYRROLIDONE CARBOXYLIC ACID.
AMIDATION (G-11 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                  MESAU
GON1 MESAU
STANDARD, PRT; 63 AA.

009163;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Progonadoliberin I precursor [Contrains: Gonadoliberin I (LH-RH I)
(Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GORH-associated peptide I]
                                                                                                                                                                                                                                                                                                                                                            (Fragment).
GNRH1 OR GNRH OR LHRH,
GASOCXICCEUS auratus (Golden hamster).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE I (BY
                                                                                                                 DB 1; Length 61;
0.0033;
hes 0; Indels
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                                                                                           63962A1AE319B8F0 CRC64;
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                                                                                                                                             0; Mismatches
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                                                                                                                     Score 52;
Pred. No.
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INCESTPO; IPRO02012; GARH.
INCESTPO; IPRO04079; GonadoliberinI.
Pfam; PP00446; GARH; 1.
                                                                                                                   96.3%; 2
100.0%;
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61 AA;
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                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S75918; AAB33096.1; -
PIR; 178541; 178541
InterPro; 178002012; GnRH.
InterPro; 178004079; GnadoliberinI.
PFam; PP00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
PROSITE; PS00473; GNRH; 1.
Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus; Signal; Pyrrolidone carboxylic acid.
NON TER.
SIGNAL SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY
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PROGOMADOLIBERIN I.
GONADOLIBERIN I.
GNRH-ASSOCIATED PEPTIDE I.
APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
ACTIVITY (BY SIMILARITY).
PYROLIDONE CARBOXYLIC ACID (BY
                          Сарв
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Hypothalamus;
MEDLINE=95124501; PubMed=7545971;
MAY V.J. Costa M.S. Cojed S.R.;
May V.J. Costa M.S. Of the genes encoding transforming growth
"Developmental expression of the genes encoding transforming growth
factor alpha and its receptor in the hypothalamus of female rhesus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
AMIDATION (G-16 PROVIDE AMIDE GROUP)
SIMILARITY).
                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2010 in I precursor (Contains: Gonadoliberin I (LH-RH I)
(Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GnRH I) (Luliberin I); GRRH-associated peptide I)
                                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mamalia; Butheria, Primates; Catarrhini, Cercopithecidae, Cercopithecidae, Macaca.
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                           0; Indels
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96.3%; Score 52; DB 1; I
100.0%; Pred. No. 0.0034;
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                             0; Mismatches
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7573 MW;
    Query Match
Best Local Similarity 100.
Matches 8; Conservative
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SNRH1 OR GNRH OR LHRH.
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                                                        2 HWSYGLRP
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P55247;
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Perfect score: 54	Copyright (c) 1993 - 2004 Compugen Ltd. rotein search, using sw model March 10, 2004, 08:58:53; Search time 1.82879 Seconds (without alignments) US-09-848-834A-1 54	<pre>// protein - I in on: tle: tle: irfect score:</pre>
	1 XHWSYGLRPX 10	Sequence:
		tle:
Title: US-09-848-834A-1	284.724 Million cell updates/sec	
US-09-848-834A-1	March 10, 2004, 08:58:53 ; Search time 1.82879 Seconds (without alignments)	ino ni
: March 10, 2004, 08:58:53; US-09-848-834A-1		
<pre>un on: March 10, 2004, 08:58:53; Search time 1.82879 Seconds</pre>	rotein search, using sw model	1 protein - I
ein - protein search, using sw model March 10, 2004, 08:58:53; US-09-848-834A-1	Copyrignt (c) 1993 - 2004 Compugen Ltd.	
M protein - protein search, using sw model un on: March 10, 2004, 08:58:53 ; Search time 1.82879 Seconds (without alignments) 284.724 Million cell updates/sec	Copyright (c) 1993 - 2004 Comments	

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SUMMARIES		GON1 SHEEP	GON1 MESAU	GON1 MACMU	GON1 XENLA		GON1 RANCA	GON1_PIG	GON1 HUMAN	GON1_RAT	GON1_TUPGB	GON1 ALLMI	GON1_CHICK	GON1 HAPBU	GON1 MORSA	GON1 PAGMA	GON1_SPAAU	GON1 DICLA	GON8_RANDY	GON1_CAVPO	GON1 CLAGA	GON1_ORYLA	GON1_CLUPA	YHBJ_ACTAC	GON3_ONCKE	GON3_ONCMY	GON3 ONCES	GON3_ONCMA	1				GON3_HAPBU	GON3_ORYLA
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P51921 pagrus majo. P51923 sparus aura P51917 carassius a Q92106 rutilus rut Q8Vhb5 mus musculu Q2866 archaeoglob P45377 mus musculu P59305 bifidobacte P75804 escherichia O55197 rattus norv O09047 mus musculu P25472 clostridium
GON3 PAGWA GON3 SPAAU GON3 CARAU GON3 RUTRU CAH9 MOUSE YF76 ARCFU ALD2 MOUSE ARGC BIFLO YILI ECOLI C3AR RAT C3AR RAT GAR RAT GAR RAT GAR CHOCE
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ALIGNMENTS

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0; Gaps
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                                                        GGD, S0001081; MSC7.
GGD, S0001081; MSC7.
GG, GO.0007131; P:meiotic recombination; IMP.
InterPro; IPR002066; Aldehyde_dehydr.
PFR081TE; PS00070; ALDEHYDE_DEHYDR_CST, 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GST, 1.
HYDOTHETICAL Protein; Oxidoreductase.
HYDOTHETICAL BSG 354
ACT_SITE 389
389
BY SIMILARITY.
SCOÜBNCE 644 AA; 71320 MW; 54DADDAEBZA16D4D CRC64;
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Search completed: March 10, 2004, 09:13:47 Job time : 4.92607 secs

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us-09-848-834a-2.open.rsp

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Vaudin M.;
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                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.; "The complete genome sequence of the lactic acid bacterium Lactococcus Genome Rep. 11403."; Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacceria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBL_TaxID=1360;
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"Biochemical and genetic characterization of PepF, an oligopeptidase from Lactococcus lactis."; J. Biol. Chem. 269:32070-32076 (1994).
                                                                                                    STRAIN=NCDO 763;
MEDLINE=9732670; PubMed=9209029;
MEDLINE=9732670; PubMed=9209029;
Mardi M., Renault P., Monnet V.;
"Duplication of the pepF gene and shuffling of DNA fragments on the lactose plasmid of Lactococcus lactis.";
-1. Function: Hydrolyzes peptides containing between 7 and 17 amino acids with a rather wide specificity.
-1. COPACTOR: Bain a lather wide specificity.
-1. COPACTOR: Bains 1 zinc ion (By similarity).
-1. SIMILARITY: Belongs to peptidase family M3.
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C8B5C519FFA2F787 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligoendopeptidase F homolog (EC 3.4.24.-).
PEPF OR LL1727.
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284 RYIELRKKILGITDL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z3252; CAA83534.1; -.
EMBL; X59798; CAA68133.1; -.
PIR; A55485; A55485.
MERCPS; M03.007; -.
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MEDLINE 94378003; PubMed=8091229;
MEDLINE 94378003; PubMed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Fulton L., Gattung S., Gaisel C., Kirsten J.,
Kucaba T., Hillier L.W., Jier M., Johnston L., Langston Y.,
Latrealle P., Louis E.J., Macril C., Mardis E., Nenezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevackis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLIK, SUBSAU, SUBCO1567; Peptidase_M3.

InterPro, IPRO01567; Peptidase_M3.

Frant, PF01432; Peptidase_M3.

INTERPAUS, TIGRO0481; PepFi 1.

Hydrolase; Metalloprotease; Zinc, Complete proteome.

Hydrolase; Metalloprotease; Zinc, Complete proteome.

ACT SITE 388 38 BY SIMILARITY.

ACT SITE 388 38 BY SIMILARITY.

METAL 394 394 ZINC (CATALYTIC) (BY SIMILARITY).

METAL 394 SIMILARITY.

SEQUENCE 601 AA; 69883 MW, 045E6873F10FE19A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypochetical aldehyde-dehydrogenase like protein in FILL-VMA10 intergenic region (EC 1.2.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 265:2077-2082(1994).
-!- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40; DB 1; Length 601;
Pred. No. 17;
specificity (By similarity).
                                    COFACTOR: Binds 1 zinc ion (By similarity) SIMILARITY: Belongs to peptidase family M3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE006403; AAK05825.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 RYIELRKKILGITDL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 QYIKANSKFIGITEL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; G86840; G86840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YHJ9 YEAST
P38694;
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                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN=ATCC 27343 / Kid;

STRAIN=B8142249; PubMed=3481422;

Ohkubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;

"The ribosomal protein gene cluster of Mycoplasma capricolum.";

Mol. Gen. Genet. 210:314-322 (1987).

-! FUNCTION: This small ubiquitous enzyme is essential for maintenance and cell growth.

-! CATALYTIC ACTIVITY; ATP + AMP = ADP + ADP.

-! SUBUNIT: Monomer Elys similarity).

-! SUBCELLOLAR LOCATION: Cytoplasmic.

-! SINILARITY: Belongs to the adenylate kinase family.
                                                                                                Bacteria: Firmicutes: Mollicutes: Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Plasmid pLP763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=NCDO 763;
MEDLINE=95096044; PubMed=7798200;
Monnet V., Nardi M., Chopin A., Chopin M.-C., Gripon J.-C.;
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 1; Length 213; Pred, No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fIGGELANDS,

FIGURATES, PSCOLI3; ADENILA.

Transferase, Kinase, ATP-binding,

Transferase, 7

15

ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
PEFI LACLC
ID PEFI LACLC
STANDARD; PRT; 601 AA.
AC E54124; P94880;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DF 01:goendopeptidase F, plasmid (EC 3.4.24.-).
GN PEFI OR PEFF
OS Inachid pLP763.
OC Bacteria; Firmicutes; Lactobacillales; Streptococo OX NOSI TAXID=1359;
RN 11
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-NCDO 763;
RX MEDLINE-55086044; PubMed=7798200;
RX MEDLINE-55086044; PubMed=7798200;
RA MODDLE V., Nardi M., Chopin A., Chopin M.-C., Gri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X06414; CAA29724.1; --
FIR; S02631; KIYYC.
HAMAP; ME 00235; -; 1.
INTECPEO; IPRO06259; Adenylate.
INTECPEO; IPRO06859; Adenylate.
INTECPEO; IPRO07862; ADK.
INTECPEO; IPRO07862; ADK.
INTECPEO; IPRO07862; ADK.
INTECPEO; IPRO0994; ADK. I.I.
FRINTS; PRO0194; ADENYLTKNASE.
FOODOM: PD0006657; Adenylate. Kin; 1.
TIGREAMS; TIGRO1351; adk; 1.
FROSITE; PS00113; ADENYLATE KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 IDYFKTNSKFIEI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MOYIKANSKFIGI 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 61.5
les 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWIS outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.;
"Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I- FUNCTION: Converts holo-ACP to apo-ACP by hydrolytic cleavage of the phosphopantetheine prosthetic group from ACP (By similarity).
-!- CATALYITC ACTIVITY: Holo-[acyl-carrier protein] + H(2)0 = 4'-phosphopantetheine + apo-[acyl-carrier protein].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINERG / KW20.' ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherry B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
McKenney K., Shirley R., Liu L.-I., Glodek A., Kalley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Wicherback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehn C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 41, Last annotation update)
Probable acyl carrier protein phosphodiesterase (EC 3.1.4.14) (ACP phosphodiesterase).
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=96186898; PubMed=6635745;
Chandler M.S., Smith R.A.
"Chandler M.S., Smith R.A.
"Characterization of the Haemophilus influenzae topA locus: DNA topoisomerase I is required for genetic competence.";
Gene 169:25-31(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                      Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.6%; Score 40; DB 1; Length 194;
53.3%; Pred. No. 5.4;
iive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_01216; -; 1.
InterPro; IPR003680; NADHGh_2.
Pfam, PF02525; Plavedome.
Hydrolase; Complete proteome.
SEQUENCE 194 AA; 21208 MW; A8AEC9D00829522C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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P10251;
01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                   Bacteria, Proteobacteria, Gam
Pasteurellaceae, Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, U20964; AAC43728.1; -. EMBL, U32816; AAC23013.1; -. PIR, G64026; G64026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 OYIKANSKFIGITEL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 269:496-512(1995).
                                                                                                                                                                          Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                     NCBI_TaxID=727,
                                                                                                                                                    ACPD OR HI1366
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Gaps

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Best Loc Matches

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us-09-848-834a-2.open.rsp

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V120_HSVSA
ID _V120 1
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TION:

MEDLINE=21992816; PubMed=11997336;

A Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,

A Chen Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

A complete sequence of T. tengeongensis genome. ";

A complete sequence of T. tengeongensis genome. Tengeongensi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 41, Last sequence update)
2-isopropylmalate synthase 2 (EC 2.3.3.13) (Alpha-isopropylmalate synthase 2) (Alpha-IPM synthetase 2).
LEUA2 OR TIE0472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1; Length 204;
Pred. No. 3.7;
5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermoanaerobacter tengcongensis.
Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales,
Thermoanaerobacteriaceae, Thermoanaerobacter.
                                                                                                                                                                             HAWAP, MF 00219; -; 1.
InterPro; IPR006680; Amidohydro 1.
InterPro; IPR002195; Pept M38 nph.
Pfan; PF01979; Amidohydro 1; 1.
PROSITE; P800482; DIHYDROGROTASE 1; PARTIAL.
PROSITE; P800483; DIHYDROGROTASE 2; 1.
Pyrimidine biosynthesis; Hydrolase; Metal-binding; Zinc.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                            34 34 2INC 2 (BY SIMILARITY).
107 107 ZINC 1 (BY SIMILARITY).
204 AA; 22899 MW; 9DBOB6C9B834B310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           384 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP; MF_01025; atypical; 1.
InterPro; IPR002034; AIPWHGit_synth.
InterPro; IPR00891; HMGL-like.
Pfam; PF00682; HMGL-like; 1.
                                                                                                                                                          EMBL; AF175466; AAD50307.1; ALT_INIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.9%;
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les 6; Conserv
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QBRCF9;
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Matches
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Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Biesinger B.,
Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B.,
Honess R.W.;
                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 1; Length 899;
Pred. No. 17;
4; Mismatches 3; Indels
                                                                                                 Score 41; DB 1; Length 384;
Pred. No. 7.1;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           899 AA; 103350 MW; F1429B3770A2885E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Primary structure of the herpesvirus saimiri genome."; J. Virol. 66:5047-5058(1992).
PROSITE; PS00815; AIPM_HOMOCIT_SYNTH 1; 1.
PROSITE; PS00816; AIPM_HOMOCIT_SYNTH_2; 1.
Leucine biosynthesis; Transferase; Complete proteome.
SEQUENCE 384 AA; 42404 MW; 095310F2C0E4AADD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Herpesvirus saimiri (strain 11).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
NCDI_TaxID=10383;
                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Capsid assembly protein 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR008643; Herpes_ORF63. Pfam; PF05765; Herpes_ORF63; 1.
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EMBL; M86409; AAA46139.1; -.
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Best Local Similarity 50...
T; Conservative
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                                                                                             Ouery Match
Best Local Similarity 54.5
Best Local Similarity 64.5
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                                                                                                                                                                                                                                   214 VKAGAKEVĠVT 224
                                                                                                                                                                                             4 IKANSKFIGIT 14
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ACPD HAEIN
ID ACPD HAEIN
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AA; 196174 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fransmembrane, GPI-anchor
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       (Potential)
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Q9S3<u>S</u>1;
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Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;
"Merozoite surface protein sequence from the Camp strain of the human malaria parasite plasmodium falciparum.";
Nucleic Acids Res. 16:1206-1206 (1988).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                  (Potential).
-!- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 4
kDa and 19 kDa antigens which are the major surface antigens of
merozoites. The maturation take place during schizont.
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-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Mercozoite surface protein 1 precursor (Mercozoite surface antigens)
(PMMSA) (GP195).
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major merozoite surface antigen (gp195) of the Uganda-Palo Alto
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DDBAD45FA352BCF3 CRC64;
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PIR; A23386; SAZQGM.
InterPro; IPR006209; EGF_like.
Pfam, PF00008; EGF_l.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1726;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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MEROZOTTE STRFACE PROTEIN 1.

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Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,
Siddigui W.A.;
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es 9; Conserv
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NCBI_TaxID=57270;
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MSP1_PLAFP
ID MSP1_PLAFP
AC P50495;
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or send an email to license@isb-sib.ch).
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Dini inhibits transcription of Serratia marcescens nuclease.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: (S)-dihydroorotate + H(2)0 = N-carbamoyl-L-
PTM: Merozoite surface antigen contain the sequence of 83 kDa, 4 kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont.
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Enterobacteriaceae; Serratia.
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InterPro; IRR066209; EGF_like.
Pfam; PR00008; EGF_1.
Malaria; Merozoite; Polyprotein; Repeat; Signal, Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1726;
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--- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
--- PATHWAY: Pyrimidine biosynthesis; third step.
--- SUBUNIT: Homodimer (By similarity).
--- SIMILARITY: Belongs to the DHOase family. Subfamily 1.
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MENCOLTE SURFACE PI
N-LINKED (GLCNAC.)
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16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2003 (Rel. 42, Last annotation update)
Dihydrocrotase (EC 3.5.2.3) (DHOase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42.5; DE Pred. No. 17; 4; Mismatches
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Bone N., Hyde J.E., Scaife J., Certa U.,
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les 9; Conservative
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     Goman M.,
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ID MSP1_PLA
AC P04934;
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MEDLINE=88011243; PubMed=3079521;
Tanabe K., Mackay M., Goman M., Scaife J.G.;
"Allelic dimorphism in a surface antigen gene of the malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                              PIM: Merozoite surface antigen contain the sequence of 83 kDa, kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont.
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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Pfam; PF00008; EGF; 1.
Malaria, Merocoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Neb _ TaxID=70153;
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 17
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MEDLINE=86136024; PubMed=3004972;
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PIR; AS4498; AS4498.
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1701 AA;
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les 9; Conserv
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P08569;
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MSP1_PLAFM
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MEDLINE=86205236; PubMed=3517809;
Weber J.L., Laininger W.M., Lyon J.A.;
Wariation in the green encoding a major merozoite surface antigen of the human malaria parasite plasmodium falciparum.";
Nucleic Acids Res. 14:3311-3323(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                (Potential).
-!- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 4 kDa and 19 kDa antigens which are the major surface antigens of merozoites, The maturation take place during schizont.
Stunnenberg H., Bujard H., "Polymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985), -i- SUBCELIULAR LOCATION: Attached to the membrane by a GPI-anchor
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01-MAR-1989 (Rel. 10, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (P195).
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(POTENTIAL).
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InterPro; IPR006209; EGF_11ke.
Pfam; PF000008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
VCBI_TaxID=5835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193768 MW; 3FC2EC59AF96EA98 CRC64;
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Pred. No. 17;
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MEDITARE-8814299; PubMed=2449612;
MEDITARE-8814299; PubMed=2449612;
PETETSON M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G.,
Brown G.V., Anders R.F., Kemp D.J.;
"Variation in the precursor to the major merozoite surface antigens
of Plasmodium falciparum.";
of Plasmodium falciparum.";
Mol. Blochem. Parasitol. 27:291-302(1988).
                                                                                                                                            -!- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 4 kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont.
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01-JAN-1990 (Rel. 13, Last sequence update)
01-GT-1996 (Rel. 34, Last amnotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
                          Tolle R., Bujard H., Cooper J.A.;
"Plasmodium falciparum: variations within the C-terminal region of merozoite surface antigen.";
Exp. Parasitol. 81:47-54(1995).
-i. SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                             EMBL, M35727; AAA29715.1; -.
EMBL; Y00087; CAA68280.1; -.
EMBL; Z35326; CAA64555.1; -.
INTELPO; INTEROGO209; EGF_like.
Pfam; PF00008; EGF, 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MENCROLTE SURFACE PROTEIN 1.
MEMBRANE ANCHOR (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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Best Local Similarity 60.0°
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P13819;
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Hatfull G.F., Sarkis G.J.;
"DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
Mol. Microbiol. 7:395-405(1993).
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MEDLINE=88166657; PubMed=3327688;
Certa U., Rotmann D., Matile H., Reber-Liske R.;
A naturally occurring gene encoding the major surface antigen precursor p190 of Plasmodium falciparum lacks tripeptide repeats.";
EMBO J. 6:4137-4142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSPI_PLAF3 STANDARD; PRT; 1682 AA.
1915361, Q25321;
01-FDB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
Mercozoite surface protein 1 precursor (Mercozoite surface antigens)
(PMMSA) (P190).
                                                                                                                                                                                                                                                                                                                                                                         Mycobacteriophage L5.
Nylunges; daDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
L5-1ike viruses.
NCBI_TaxID=31757;
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBL_TaxID=5834;
                    Length 1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.7%; Score 44; DB 1; Length 66; 57.1%; Pred. No. 0.33; 4; Indels tive 2; Mismatches 4; Indels
                                                           Indels
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PIR; S31029; S31029.
PIR; S31029; S37029.
                    Query Match
100.0%; Score 79; DB 1; I
Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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hes 8; Conservative
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Q05301;
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Gaps

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TETANUS TOXIN LIGHT CHAIN.
TETANUS TOXIN HEAVY CHAIN.
ZINC (CATALYTIC) (BY SIMILARITY).
EV SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
POTENTIAL.
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DISULFID
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RNE outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                              SYMADLODREVIN 2.

CORACTOR, BINGS 1 zinc ion per subunit (By similarity).

SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO
YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE
AND ARE NON-TOXIC AFTER SEPARATION.

MISCELLANDSOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
GANGLIOSIDE RECEPTORS.
                                                                                                                                                     identification of substrate.

Mobiline 33063293; Pubmed=1331807;

Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P., Dasgupta B.R., Montecucco C.;

Trefanus and botulinum-B neurotoxins block neurotransmitter release by proteolytic cleavage of synaptobrevin.";

Nature 359:832-835(1992).
                                                                                                                                                                                                                                                 ם.ם
                                                                                                                "Tetanus toxin is a zinc protein and its inhibition of
neurotransmitter release and protease activity depend on zinc.";
EMBO J. 11:3577-3583(1992),
                                   Krieglstein K.G., Henschen A.H., Weller U., Habermann E.;
"Limited proteolysis of tetanus toxin. Relation to activity and
identification of cleavage sites.";
Eur. J. Biochem. 202:41-51(1991).
                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.
MEDLINE=97475217; PubMed=9334741;
Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt
                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Hydrolysis of 76-Gln-|-Phe-77 bond in
                                                                              IDENTIFICATION AS ZINC-PROTEASE.
SDILONE-93010948; PubMed-1396558;
SChiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
Montecucco C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR008985; ConA like lec_gl.
InterPro, IPR002160; Kunitz_legume.
InterPro, IPR066025; Pept_M_Zn_BS.
        [6]
PARTIAL SEQUENCE.
MEDLINE=92037649; PubMed=1935979;
J. Biochem. 188:39-45(1990)
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EMBL; X05214; CAA2564.1; --
EMBL; AF52809; AA027454.1; --
EMBL; MI2739; AAA22282.1; --
PIR; A25689; BTCLIN.
PDB; 1AF9; 29-ARR-98.
PDB; 1ABD; 14-OCT-98.
PDB; 1DBD; 27-MAR-00.
PDB; 1DIW; 24-MAR-00.
PDB; 1PV3; 05-SEP-01.
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chlamydia p
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rhodobacter
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13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 02, Last annotation update)
Tetanus toxin precursor (EC 3.4.24.68) (Tencoxylysin) [Contains:
Tetanus toxin light chain (Tetanus toxin chain L); Tetanus toxin heavy
Chain (Tetanus toxin chain H)].
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MEDLINE=86085672; PubMed=3510187;
Rairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;
"Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in Escherichia coll.";
J. Bacteriol. 165:21-27(1986).
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Plasmid pE88, and Plasmid 75 Kbp.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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MEDLINE=22457253; PubMed=12552129;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A., Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eisel U., Jarausch W., Goretzki K., Henschen A., Engels J., Weller U., Hudel M., Habermann E., Niemann H.;
"Tetanus toxin: primary structure, expression in E. coli, and homology with botulinum toxins.";
EMBO J. 5:2495-2502(1986).
                 P21770
P13877
P57439 D091577
Q02773
P33659
P31179
P31179
P11410
P40009
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STRAIN=CN1911; PLASMID=75 KDp;
MEDLINE=87040747; PubMed=3774547;
Fairweather N.F., Lyness V.A.;
"The complete nucleotide sequence of tetanus toxin.";
Nucleic Acids Res. 14:7809-7812(1986).
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2ASD YEAST
RRP3_INCBE
RRP3_INCJJ
Y3S8_BUCAI
CSG_XENLA
MIP_CHLDA
YD01_CLOAB
NADA_CYAPA
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NIFN_RHOCA
G6PD_PICJA
YND1_YEAST
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MEDLINE=87053814; PubMed=3536478;
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744012888449
74401388888
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 Clostridium.
NCBI_TaxID=1513;
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             GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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3 YIKANSKFIGITEL 16 ||||||||| 57 XIKYNEKFKGTTTL 70 q

Search completed: March 10, 2004, 09:16:40 Job time: 7.03937 secs

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KiFrommer, G.; Schuh, R.; Jdckle, H.
submitted to the EMBL Data Library, November 1993
A; Description: Localized expression of a novel micropia-like element in the blastoderm A; Reference number: $38635
A; Accession: $38635
A; Accession: S28635
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-1333 < FRO>
A; Cross-references: EMBL: Z27119; NID: 9415797; PID: 9415798
A; Cross-references: EMBL: Z27119; NID: 9415797; PID: 9415798
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: G48677
R;Tassignon, J; Brait, M.; Jamila, I.; Urbain, J; Gottlieb, P.; Brown, A.; Hasemann, Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A;Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibod. A;Reference number: A48677; MUID:94022404; PMID:8415731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GB:AE005174; NID:g12515873; PIDN:AAG56816.1; GSPDB:GN00145; UWGP:Z. A,Experimental source: strain 0157:H7, substrain EDL933 C;Genetics: A,Genetics: A,Genetics: 22873
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Potamousis,
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C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-
C; Accession: D85794
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; R
11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1333;
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ed. No. 40;
Mismatches 4
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51.9%; Score 41; DB 2;
Best Local Similarity 64.3%; Pred. No. 5.6;
Matches 9; Conservative 0; Mismatches
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Pred. No. 3.6;
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A, Cross-references: FlyBase: FBgn0014947
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Best Local Similarity 46.7
Matches 7; Conservative
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Matches 8: Conser
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A;Molecule type: DNA
A;Residues: 1-79 <STO>
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A; Accession: 806361
A; Molecule type: DNA
A; Residues: 1104-1726 ewrez>
A; Cross-references: EMBL:X03831
C; Comment: The merozoite stages of different strains have strain-specific surface antige
C; Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The me
C; Superfamily: major merozoite surface antigen
C; Koywords: glycoprotein; merozoite; surface antigen
C; Koywords: glycoprotein; merozoite; surface antigen
C; Koywords: glycoprotein; merozoite surface antigen #status predicted <AMT>
F; 20-1726/Product: major merozoite surface antigen #status predicted <AMT>
F; 20-1726/Product: major merozoite surface antigen #status predicted <AMT>
F; 20-1726/Product: major merozoite surface antigen #status predicted <AMT>
F; 20-1726/Product: Major merozoite surface antigen #status predicted <AMT>
F; 20-1726/Product: Major merozoite surface antigen #status predicted <AMT>
F; 20-1726/Product: Major Ma
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R;Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
R;Chang, S.P.; Kramer, K.J.; 1988
A;Title: Plasmodium falciparum: gene structure and hydropathy profile of the major meroz A;Reference number: A45948; MUID:89005525; PMID:3049134
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A; Residues: 1-1104 <WEB1>
A; Residues: 1-1104 <WEB1>
A; Cross-references: ENBL:X03831
B; Weber, Jil.; Sim, B.K.L.; Lyon, J.A.; Wolff, R.
Nucleic Acids Res. 16, 1206, 1988
A; Title: Merozoite surface protein sequence from the Camp strain of the human malaria |
A; Reference number: S06361
A; Molecule type: DNA
A; Molecule type: D
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A45948
major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
C.Species: Plasmodium falciparum
C.Pace: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C.Accession: A45948
                                                                              - malaria parasite (Plasmodium falciparum)
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                                                                                            Nighternate names: 195K glycoptotein
Cispecies: Plasmodium falciparum
Cispecies: Plasmodium falciparum
Cipate: 30.58p-1987 #sequence_revision 31-Mar-1991 #text_change 09-Jun-2000
Cipate: 30.58p-1987 #sequence_revision 31-Mar-1991 #text_change 09-Jun-2000
Signer, Ji., Leninger, W.M.; Lyon, J.A.
Nucleic Acids Res. 14, 3311-3323, 1986
AiTitle: Variation in the gene encoding a major merozoite surface antigen of the Air facession: A23386; MUID:86205236; PMID:3517809
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blastopia polyprotein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
C;Accession: $38635
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Pred. No. 42;
4; Mismatches
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-1726 < CHA>
A,Cross-references: GB M37213
A,Cross-references: GB M37213
CS.Superfamily: major merozoite surface antigen
C,Keywords: surface antigen
                                                                                       surface antigen precursor
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QFVKSNSKVITGLTE 1040
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Best Local Similarity 60.0.
-hag 9; Conservative
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Best Local Similarity 60.0
Matches 9, Conservative
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A,Gene: MSA1
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
                     A;Cross-references: EMBL:X61930
A;Experimental source: isolate RO-71
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A;Residues: 1-1086 <OLA>
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                                                                                 Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (st
N,Alternate names: 190K protein; polymorphic schizont antigen
C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Melanochromis auratus
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
C;Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 05-Nov-1999
R;Ono, H: 07-Huigin, C: Tichy, H: Klein, J.
Mol. Biol. Evol. 10, 1060-1072, 1993
A;Reference number: A48209; MulD:94018589; PMID:8412649
A;Accession: I50966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Gene: 227A; 194D
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42.5; DB 2; Length 82; Pred. No. 2; 5; Mismatches 2; Indels
                        WHC class II beta chain - Melanochromis auratus (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB:L17456; NID:g309011; PID:g309012
                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-82 <ONO>
                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: 150983
A,Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen
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31 MEYIRFDSSVGKFVGFTQL 49
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Best Local Similarity 47.4%;
Matches 9; Conservative
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|::|:|||||||983 QFVKSNSKVITGLTE 997
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Best Local Similarity 60.0
Matches 9; Conservative
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A; Residues: 1-82 < ON2>
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150966
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microm merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (Cypecies: Plasmodium falciparum alciparum falciparum fal
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C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen
C;Keywords: surface antigen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1701/Product: major merozoite surface antigen #status predicted <MAT>
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                                                        53.8%; Score 42.5; DB 2; Length 1086; 60.0%; Pred. No. 26; tive 4; Mismatches 1; Indels 1.
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Query Match
Best Local Similarity 60.0%
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Best Local Similarity 60.00
Best Local 9, Conservative
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A;Residues: 1-1701 <1
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diamine N-acetyltransferase (EC 2.3.1.57) [imported] - Lactococcus lactis subsp. lactis NAIterrate names sparmidine acetyltransferase (Species: Lactococcus lactis acetyltransferase (Species: Lactococcus lactis actis lactis acetyltransferase (Species: Lactococcus lactis acetyltransferase) (Species: Lactococcus lactis acetyltransferase) (Species) A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C, Superfamily: Escherichia coli ribosomal-protein-alanine N-acetyltransferase rimJ
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A;Cross-references: GB:AE005176; PID:g12724622; PIDN:AAK05713.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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S.Species: ateline herpesvirus 3

A;Variety: strain 73

C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
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submitted to the EMBL Data Library, August 1998
A, Description: Primary structure of the herpesvirus ateles genome. A, Reference number: 222274
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Pred. No. 18; 4; Indels
1; Mismatches 4; Indels
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Pred. No. 3.6;
1; Mismatches 3; Indels
                                                                                                                                                                                                   55.7%; Score 44; DB 2; Length 66; 57.1%; Pred. No. 0.86;
                                                                                                                                                                                                                                                                              4; Indels
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A,Molecule type: DNA
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A;Cross-references: EMBL:AF083424; PIDN:AAC95587.1
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                                                                                                                                                                                                                                                                                                                                                             3 YIKANSKFIGITEL 16
                                                                                                                                                                                                                                                                                                                                                                                                                                        50 YIKRNGKFVGTWEV 63
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                                                                                                                                                                          Query Match
Best Local Similarity 57.1%
Best Local 8; Conservative
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Best Local Similarity 69.2
Matches 9; Conservative
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Best Local Similarity 64.3<sup>3</sup>
Matches 9, Conservative
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                                                                                           A;Gene: 84
A;Start codon: GTG
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F;234/Active site: Glu #status predicted
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A,Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin. A,Feference number: 869348; MUD:95262688; PMID:7744050
A,Accession: 869348
A,Accession: 869348
A,Residues: 2-31 CDEF-
C,Comment: The source of this protein was an extrachromosomal plasmid. Grayment: The precursor is cleaved by endogenous proteinase activity to form light (fra dual chains are not toxic when separated): The amino end of the heavy chain (fragment B). Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to ganglid C,Comment: This potent neurocoxin binds to peripheral neuronal synapses, is internalized presymptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 244;
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10; Conservative
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Best Local Similarity
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SECURNCE FROM N.A.
STRAIN=C57BL/6J, TISSUE=Head;
STRAIN=2049374; PubMed=11042159;
MEDLINE=2049374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Franci P., Subbraction of Cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                    STRAIN=CS7EL/6J; TISSUE=Head; MEDINEE-22354681; PubMed=12466851; The PRANTOM CONSORTIUM CONSORTIUM CONSORTIUM CONSORTIUM FANDY CONSORTIUM FARENCE EXPLORATION Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; the Fands transcriptome based on functional annotation of 60,770 full-length CDNAs."; Nature 420:563-573(2002).
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C STRAIN=2050913; PubMed=11076861;
Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
A MeDLINE=2050913; PubMed=11076861;
A Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
A Konno H., Akiyama J., Nakamura S., Hazama M., Nishine T., Harada A.,
A Mamamoto R., Matsumoto H., Sakaguchi S., Itsagami T., Kashiwagi K.,
A Yamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumixa S., Kawai J.,
A Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunixa S., Kawai J.,
RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
C Genome Res. 10:1751-1771(2000).
           Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanaqaki T., Hara A., Hayatsu N., Hiramoto K., Hiracoka T., Hori F., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Mishi K., Nomura K., Numazaki R., Ohno M., Koya S., Kurihara C., Okazaki Y., Mishi K., Nomura K., Numazaki R., Ohno M., Sono H., Sasaki D., Shibata K., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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PS01179; PID; 1.
291 AA; 32802 MW; 91FF3F41CD0BC6F2 CRC64;
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GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR006020; PTB_PID.
Pfam; PF00640; PID; 1.
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MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.,
High-efficiency full-length; cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE-Head;
STRAIN=CSTBL/66; TISSUE-Head;
MEDLINE=21085660; Pubmed=11217851;
RIKEN FANYOM CONSCITTUM;
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STRAIN=C57BL/6J; TISSUE=Head;
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Query Match Best Local Similarity

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Search completed: March 10, 2004, 09:25:22 Job time : 18.8132 secs
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11 YIPYNAKFLGSTEV 24
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Van Sinderen D., van de Guchte M., Seegers J.F.M.L., Fitzgerald G.F., van Sinderen D., van de Guchte M., Seegers J.F.M.L., Fitzgerald G.F., Molecular analysis of the temperate lactococcal phage Tuc2009."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF109974, AAD31103.1;
GO; GO:00033677; F:DNA binding; IEA.
GO; GO:00033677; F:DNA methyltransferase activity; IEA.
GO; GO:000306; P:DNA methyltrini, IEA.
InterPro; IPR002294; NoTM methylation; IEA.
InterPro; IPR002941; Met trans_CN4.
InterPro; IPR002941; NoF/N4 Mtase.
FRAM; PR01555; No N4 Mcase; I.
FRANTS; PR00506; D21N6MTFRASE.
FRINTS; PR00508; S21N4MTFRASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis bacteriophage Tuc2009.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
VCBI_TaxID=35241;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
13 days embryo head cDNA, RIKEN full-length enriched library,
clone:3110030A04 product:CED-6 protein homolog.
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Pred. No. 22;
2; Mismatches 4; Indels
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GO:0008170, F:N-methyltransferase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                              OSXJE8;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative methylase.
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                 GO, GO: 0006506; P:DNA methylation; IEA.
InterPro: IPR001295; D21N6 mtfrase.
InterPro: IPR001091; Met_trans_CN4.
InterPro: IPR001091; Met_Knase.
Pfam: PF01555; NS N4 Mtase.
PRINTS; PR00506; D21N6MTFRASE.
PRINTS; PR00508; S21N6MTFRASE.
SEQUENCE 250 AA; 28744 MW; 725EA3B2B:
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Local Similarity 57.1%;
les 8; Conservative
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SEQUENCE 252 AA;
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SEQUENCE FROM N.A.
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MEDLINSE-2123186; PubMed=11337471;
MEDLINSE-2123186; PubMed=11337471;
BOICTIN A., WITCKER P., Mauger S., Jaillon O., Malarme K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis 11403."
Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
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MEDLINE=2008830; PubMed=10620678;
Stanley E., Walsh L., van der Zwet A., Fitzgerald G.F.,
van Sinderen D.;
"Identification of four loci isolated from two Streptococcus
"Identification of four loci isolated from two Streptococcus
thermophilus phage genomes responsible for mediating bacteriophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus thermophilus bacteriophage 7201.
Viruses, daDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=112023;
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PIR, G86226; G86826.

POR G0.0004145; F.idamine N-acctyltransferase activity; IEA.

G0; G0.0004145; F.itansferase activity; IEA.

InterPro; IPR00182; GCN5acetyl_trans

Fransferase; Complete protecome.

SEQUENCE 180 AA; 21022 MW; 6DBD148524C0DF3C CRC64;
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Pred. No. 15;
1; Mismatches 3; Indels
        Indels
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01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Spermidine acetyltransferase (BC 2.3.1.57).
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                                        2 OYIKANS --- KFIGITEL 16
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Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;

Grimholt U., Olsaker I., de Vries Lindstrom C., Lie O.;

"A study of polymorphism in the MHC class II beta 1 and MHC class II

"In alpha 2 domain exons of Atlantic salmon (Salmo.salar).";

Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.

R GO, GO:0016021; C. integeral to membrane; IEA.

GO, GO:0016021; F.MHC class II receptor activity; IEA.

R GO, GO:0019884; P:antigen presentation, exogenous antigen via M. ..; IEA.

R GO, GO:0019885; P:antigen presentation, exogenous antigen via M. ..; IEA.

R GO, GO:0019889; MHC II beta.

R Fam; PRO0969; MHC II beta.

R Probom; PD000328; MHC II beta.
                                                                                                                                                                                                                                                                                                                 MEDLINE=20087226; PubMed=10618395; Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M., Cavalier-Smith T., Maier U., Douglas S.; Maier Drotein and centrosomal genes, a tRNA intron, and odd telomeres in an unusually compact eukaryotic genome, the cryptomonad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.7%; Score 44; DB 10; Length 546; 50.0%; Pred. No. 31; ive 6; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDIJNE=21223349; PubMed=11323671;
MEDIJNE=21223349; PubMed=11323671;
Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., I bouglas S., Zauner S., Fraunholz M., Maier U.;
"The highly reduced genome of an enslaved algal nucleus.";
"The highly reduced genome of an enslaved algal nucleus.";
"The highly reduced genome of an enslaved algal nucleus.";
"The highly reduced genome of an enslaved algal nucleus.";
"The highly reduced genome of an enslaved algal nucleus.";
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"The highly reduced genome of an enslaved algal nucleus.";
"The highly reduced genome of an enslaved algal nucleus.";
"The highly reduced genome of an enslaved algal nucleus.";
"The highly reduced a
                           O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Guillardia theta (Cryptomonas phi).
Eukaryota, Cryptophyta, Cryptomonadaceae, Guillardia.
NCBL TAXID=55529;
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01-UTN-2003 (TrEMBLrel. 24, Last annocation update)
(DB03) WHC class II beta 1 (Fragment).
Salmo salar (Atlantic salmon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleomorph.";
Proc. Natl. Acad. Sci. U.S.A. 97:200-205(2000)
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546 AA
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445 FIKSNSRFMRLTEI 458
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   PRELIMINARY;
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TISSUE-Leukocyte;
MEDLINE-93170890; PubMed-8436418;
MEDLINE-93170890; PubMed-8436418;
Hordvik I., Grimholt U., Fosse V.M., Lie Y., Endresen C.;
"Cloning and sequence analysis of cDNAs encoding the MHC class II is "Claning and sequence analysis of cDNAs encoding the MHC class II immunogenetics 37:437-441 (1993).
EMBL; X70166; CAA49725.1; -.
EMBL; X70166; CAA49725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmo salar (Atlantic salmon).
Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Protecanthopterygii, Salmoniformes, Salmonidae, Salmo.
GO, GO:0045012; F:MHC class II receptor activity; IEA.
GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
GO; GO:0019886; P:antigen processing, exogenous antigen via M. .
GO; GO:000595; P:immune response; IEA.
InterPro; IPRO00353; MHC_II_beta.
Probom; PRO0069; MHC_II_beta, I.
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R GG; GO:0016021; C:integral to membrane; IEA.

R GG; GO:0016804; P:antigen presentation, exogenous antigen; IEA.

R GG; GO:0019804; P:antigen presentation, exogenous antigen; IEA.

R GG; GO:0019804; P:antigen processing, exogenous antigen via M.

R GG; GO:00108055; P:antigen processing, exogenous antigen via M.

R DinterPro; IPR00359; IGG ol.

R InterPro; IPR00359; IGG ol.

R Pfam; PF000047; ig; 1.

R Pfam; PF000047; ig; 1.

R PFODOM; PR000058; MHC II beta; 1.

R PADOM; PR0000518; MHC II beta; 1.
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                                                                                                                                                                                                                                                                                                                                                      DB 7; Length 86;
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Glycoprotein; MHC II; Transmembrane.
SEQUENCE 244 AA; 27449 MW; 496CB9EA9D73765C CRC64;
                                                                                                                                                                                                                                                                      86
9912 MW; E5097729F681F149 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          031590;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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55.6%; Pred. No. 11;
tive 3; Mismatches
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Matches 10; Conservative
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MHC-SASA CLASS II B.
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86
86 AA;
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Best Local Similarity

RESULT 10 Q9XG37

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MEDLIKE=21383619; PubMed=11491536;

MEDLIKE=21383619; PubMed=11491536;

MEDLIKE=21383619; PubMed=11491536;

MITALIE Delymorphism in MHC class II B in four populations of Atlantic salmon (Salmo salar).";

Atlantic salmon (Salmo salar).";

Atlantic salmon (Salmo salar).";

MEDLIKE=25.336(5001).

EMBL; ARI04370; AAL04002.1; -..

CO; GO:0016021; C:integral to membrane; IEA.

CO; GO:0019886; P:antigen processing, exogenous antigen, IEA.

CO; GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.

CO; GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.

CO; GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.

CO; GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.

CO; GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.

CO; GO:001988; MHC_II_beta; I.

Prodom; PRO00328; MHC_II_beta; I.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_TaxID=8030;
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MEDLINE=21383619; PubMed=11491536;
Langefors A., Lohm J., Von Schantz T.;
Langefors A., Lohm J., Von Schantz T.;
Allelic polymorphism in MHC class II B in four populations of Atlantic salmon (Salmo salar).";
Immunospenetics 53:329-336(2001).
EMBL, AFI04377; AA04009.1;
GO, GO:0016021; C:integral to membrane; IEA.
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                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
MHC class II B antigen (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
MHC class II B antigen (Fragment)
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                                                                                      33 EYİRFNSTVGKFVGYTEL 50
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                           2 OYIKANS --- KFIGITEL 16
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Best Local Similarity 55.6
Matches 10, Conservative
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Q95HX4;
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Q95HY1
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The Dorschner M.O., Duris T., Phillips R.B.;

The Dorschner M.O., Duris T., Phillips R.B.;

The Dorschner M.O., Duris T., Phillips R.B.;

The Submitted (FEB.1999) to the EMBL/GenBank/DDBJ databases.

E. Submitted (FEB.1999) to the EMBL/GenBank/DDBJ databases.

The Malloude (FEB.1999) to the EMBL/GenBank/DDBJ databases.

The GO, GO:0016021; F:MMC class II receptor activity; IEA.

GO; GO:0019884; P:Antigen processing, exogenous antigen; IEA.

GO; GO:0019886; P:Antigen processing, exogenous antigen via M. .;

GO; GO:0016955; P:immune response; IEA.

The Probom; PD000328; MMC II beta.

The Probom; PD000328; MMC II beta.

The MON TER T. Transmembrane.

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Landry C., Bernatchez L.;
Landry C., Bernatchez L.;
Comparative analysis of population structure across environments are geographic scales at Major Histocompatibility Complex and microsatellite in Atlantic salmon (Salmo salar).";
L Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF373659; AAKG1882.1;
R GO; GO:0016021; F:NHC class II receptor activity; IEA.
R GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
R GO; GO:0019886; P:antigen precessing, exogenous antigen via M. ..;
R GO; GO:0019886; P:immune response; IEA.
R GO; GO:0019886; P:immune response; IEA.
R PFaDCm; PR009695; MHC_II_beta; 1.
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                                                                                      Salvelinus namaycush (lake trout).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Buteleostei,
Protacanthopterygii, Salmoniformes; Salmonidae, Salvelinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44.5; DB 7; Length 71; Pred. No. 3.3; Mismatches 2; Indels
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85 85
85 AA, 9743 MW; 3214E01AD1B66AC5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
MHC class II beta chain (Fragment).
Salmo salar (Atlantic salmon).
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
MHC class II beta 1 (Fragment).
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Best Local Similarity 55...
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Best Local Similarity 55.c.
Thea 10; Conservative
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                          NCBI_TaxID=8040;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                 Length 880;
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                                                                                                                                                                                                                                                                                                                                          Aminoacyl-tRNA synthetage, Complete proteome.
SEQUENCE 880 AA, 97887 MW, EF23ED1229B6683F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 60 ° 504F3449060940E2 CRC64;
GO:0001676; F:nucleic acid binding; IEA.
GO:0006419; P:alanyl-tRNA aminoacylation; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-UDM-2003 (TrEMBLrel. 24, Last annotation update) (DB02) MHC class II beta 1 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                   58.2%; Score 46; DB 16;
69.2%; Pred. No. 22;
artive 1; Mismatches 3
                                                                        InterPro; IPR00115; DHMAI.
InterPro; IPR00165; DHMAI.
InterPro; IPR00169; SHProte acaite.
InterPro; IPR00219; tRNA-synt_Ala.
Pfam; PF02272; DHMAI; 1.
Pfam; PF02272; DHMAI; 1.
Pfam; PF03411; tRNA-synt_Ala.
INGRPAM; TIGRO344; alas; 1.
PROSITE; PS00860; AA TRNA LIGASE II ALA; 1.
PROSITE; PS00619; THIOL_PROTEASE HIS; 1.
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Pred. No. 2.8;
3; Mismatches
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01-NOV-1999 (TrEMBLrel, 12,
01-NOV-1999 (TrEMBLrel, 12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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SEQUENCE FROM N.A.
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Q9XRJ9
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SEQUENCE FROM N.A.
STRAIN-V583 / ATCC 700802;
MEDLINE-22550857; PubMed-12663927;
Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Paulsen I.T., Paulsen J.E., Eisen J.A., Gill S.R., Heddelborg J.F.,
Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
Vamathevan J., Tran B., Upton J., Haneen T., Shetty J., Khouri H.,
Utterback T., Radune D., Kectoum K.A., Dougherty B.A., Fraser C.M.;
"Role of mobile DNA in the evolution of vancomycin-resistant
Science 299:2071-2071-2071.
Science 299:2071-2071-0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-2704745. PubMed=12886019;

Gil R., Silva F.J., Zientz B., Delmotte F., Gonzalez-Candelas F.,
Latorie A., Rusell C., Kamerbeek J., Gadau J., Hoelldobler B.,
Latorie A., Rusell C., Kamerbeek J., Gadau J., Hoelldobler B.,
Van Ham R.C.H.J., Gross R., Moya A.;
Of reduced sequence of Blochmannia floridanus: comparative analysis
proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003).
EMBI. BX248894; CAD835681; -.
LEMBE, BX248894; CAD835681; -.
Liyase; Complete proteome.
SEQUENCE 447 AA; 49005 MW, 465B69C3273C7AC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candidatus Blochmannia floridanus.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
NCBI_TaxID=203907;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.2%; Score 46; DB 16; Length 447; 46.7%; Pred. No. 11;
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0835JB; 01-UNN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Alanyl-tRNA synthetase.
Alanyl-tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
           4.3e-05;
hes 0;
                                                                                                                                                                                                                                                                          447 AA
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           Pred. No. 4.3
Mismatches
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           Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
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Q7VQH3

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01-OCT-2003 (TERMBLE1. 25, L6

01-OCT-2003 (TERMBLE1. 25, L6

01-OCT-2003 (TERMBLE1. 25, L6

Enclase (EC 4.2.1.11).
                                                                                                                                         830 MOYIKANSKFIGITEL 845
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Best Local Similarity 46.7
Matches 7; Conservative
                                                                                            1 MOYIKANSKFIGITEL
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Q9cyd2 mus musculu Q8tzu8 pyrococcus Q8h8f3 actine her Q9ytk4 ateline her Q31453 melanochrom Q3dek4 coregonus G2594 plasmodium Q5tzt5 plasmodium Q5tzt5 plasmodium Q5tzt4 plasmodium Q25522 plasmodium Q25922 plasmodium Q25922 plasmodium Q3f64 photorhabdu Q24262 drosophila Q9dej6 coregonus Q95is3 salmo salar Q35is3 salmo salar Q35is3 salmo salar Q35is3 salmo salar Q35is3 salmo crutt Q8x466 escherichia Q8x466 escherichia Q8x466 escherichia Q8x466 escherichia Q813b2 mus musculu Q3dd7 hhermoanaer Q813b2 mus musculus Q3dd7 homo sapien Q8G148 cricetulus Q3dd7 homo sapien Q8G148 cricetulus

Q9CYD2 Q8HEZU8 Q8HEZU8 Q9YTK4 Q31450 Q9DEK4 Q9DEK4 Q25921 Q9TZT5 Q9TZT5 Q9TZT7 Q9TZT7 Q9TZT7 Q9TZT7 Q9TZT7 Q9TZT7 Q9TZT7 Q9TZ7

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Q93N27
  Q33127 clostridium
Q7Vqh3 candidatus
Q7Vqh3 candidatus
Q31585 salmo salar
Q95x19 salmo salar
Q95x219 salmo salar
Q95x4 salmo salar
Q95x4 salmo salar
Q95x9 quillardia
Q3578 salmo salar
Q96x66 lactococcus
Q9c66 lactococcus
Q9mc17 streptococcus
Q9mc17 streptococcus
Q9mc17 streptococcus
                                                                                                                                       March 10, 2004, 08:58:54; Search time 15:8132 Seconds (without alignments) 319.245 Million cell updates/sec
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   - protein search, using sw model
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sp_bacteria: *
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Gapop 10.0 , Gapext 0.5
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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Match Length DB
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ALIGNMENTS

01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
10-OCT-2003 (TrEMBLRel. 19, Last annotation update)
10-OCT-2003 (TrEMBLRel. 19, Last annotation update)
10-OCT-2003 (TrEMBLRel. 19, Last annotation update)
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10-OCT-2003 (TrEMBLRel. 19, Last annotation update)
10-OCT-2003 (TrEMBLel. 19, Last annotation update)
10-OCT-2003 (TrEMBLel. 19, Last anno Length 1310; Shumin Z., Dianliang L.;

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Shumin Z., Dianliang L.;

Shumin Z., Dianlia 150316 MW; 9EADDC914418E450 CRC64; DB 2; PRT; 1310 AA ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
PROSITE; PS00142; ZINC_PROTEĀSE; 1.
NOW_TER 1.
NOW_TER 1310 1310
SEQÜENCE 1310 AA; 150316 MW; 9EADDC914 100.0%; Score 79; S THE PROPERTY OF THE PROPERTY

Query Match

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093N27 087VQH3 087VQH3 087SJ8 095KKJ9 095KKJ9 095KKJ9 095KKJ9 095KKJ9 031578 031578 031578 031578 031578 031578 031578

27 9 8 6 7 1

Gaps

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US-10-339-52-9

US-10-339-52-9

SUBJICATION NO. US2003108559A1

SUBJICATION NO. US2003108559A1

GENERAL INFORMATION:

APPLICANT: Thomas, Lawrence J.

TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVIT:

FILE REFERENCE: TCS-411.1P US-3

CURRENT APPLICATION NUMBER: US/10/339,522

CURRENT APPLICATION NUMBER: US/10/339,522

PRIOR FILING DATE: 1995-05-01

PRIOR PLING DATE: 1995-05-01

PRIOR PILING DATE: 1999-10-17

PRIOR PILING DATE: 1999-10-17

PRIOR PILING DATE: 2001-08-30

PRIOR FILING DATE: 2001-08-30

PRIOR FILING DATE: 2001-08-30

NUMBER OF SEQ ID NOS: 9

SOFTWARE PATENTIN VERSION 3.1

SEQ ID NO 9

LENGTH: 50

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                                                                                                                                                                                                                                                                                         Length 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: vaccine peptide of the invention US-10-339-522-9
                                                                                                                                                                                                                    ; OTHER INFORMATION: vaccine peptide of the invention US-09-943-548-9
                                                                                                                                                                                                                                                                                       94.9%; Score 75; DB 9; Lalarity 100.0%; Pred. No. 1.9e-06; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 08/945,289
PRIOR FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 50
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ORGANISM: Artificial Sequence
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Matches 15, Conserva
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APPLICANT: Rittershaus, Lawrence J.
APPLICANT: Thomas. Lawrence J.
TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
FILE REFERENCE: TCS-411.1P US-1; TCs-411.1P US-2
CURRENT APPLICATION NUMBER: US/09/943,548
PRIOR APPLICATION NUMBER: 08/432,483
PRIOR PLING DATE: 1995-0-0
PRIOR PLING DATE: 1995-0-0
PRIOR PLING DATE: 1995-0-0-1
                                                                                                                                                                      LOCATION: (17). (31)
OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus toxoid precursor OTHER INFORMATION: (Tentoxylysin)
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                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
LOCATION: (32)..(37)
OTHER INPORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (38)..(46)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GnEH hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                              LOCATION: (1)..(10) OTHER INFORMATION: Amino acid sequence 1-10 of the human GRRH hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                      96.2%; Score 76; DB 9; Length 46; 93.8%; Pred. No. 1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ferring BV
TITLE OF INVENTION: Solubilised Protein Vaccines
FILE REPERENCE: F66451500
FILE REPERENCE: F66451500
CURRENT FILING DATE: 2003-04-21
FRIOR APPLICATION NUMBER: PCT/DK01/00431
FRIOR PILING DATE: 2001-10-16
FRIOR PILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PECENTIN Version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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Publication No. US20030185816A1
GENERAL INFORMATION:
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                                                                                                   LOCATION: (11)..(16)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
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Best Local Similarity 93.88
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CRGANISM: Homo sapiens
US-10-297-942-8
                                                                            NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                           US-09-848-834A-19
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CHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the COTHER INFORMATION: RH hormone linked by a spacer to amino sequence 830-844 of the 7 OTHER INFORMATION: RH hormone linked by a spacer to amino sequence 830-844 of the 7 OTHER INFORMATION: tanus toxoid precursor (Tentoxylysin)

NAME/KEY: MOD FROM CONTROL (1)...(1)

OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline

NAME/KEY: PEPTIDE

LOCATION: (1)...(10)

OTHER INFORMATION: Amino acid sequence 1-10 of the human GRRH hormone
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OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human other information of an apacer to amino acid sequence 830-844 of Tetan OTHER INFORMATION: toxoid precursor (Temtoxylysin) linked by a spacer to amino acid oTHER INFORMATION: toxoid precursor (GRH NAME/KEY: NOD RES OCHER INFORMATION: $\text{40} \)
COCHER INFORMATION: $\text{40} \)
NAME/KEY: NOD RES
LOCATION: (46).
OTHER INFORMATION: Amidated glycine or glycinamide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (17)..(31)
OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus toxoid precursor OTHER INFORMATION: (Tentoxylysin)
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llarity 93.8%; Pred. No. 7.1e-07;
Conservative 1; Mismatches 0; Indels
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Sequence 19, Application US/09848834A
Sequence 19, Application US/09848834A
Sequence 19, Application US/09848834A
PERTAIN NOT US20020006416A1
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REPRENCE: 1102865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT PILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/20,328
PRIOR FILING DATE: 2000-05-05
SOFTWARE: Patentin version 3.0
SEQ ID NO 19
LENGTH: 46
Sequence 15, Application US/09848834A

Patent No. US20020076416A1

GENERAL INFORMATION:
TYPLE OF INVENTION: Chimeric Peptide Immunogens
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047

CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT PILING DATE: 2001-05-04

PRIOR PRIOR DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin version 3.0

SEQ ID NO 15

LENGTH: 31

LENGTH: APPLICATION TOWNS: 20

SOFTWARE: Patentin Version 3.0

SEQ ID NO 15

LENGTH: APPLICATION TOWNS: 20

SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: PEPTIDE
LOCATION: (11)..(16)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (17)..(31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 15; Conserv
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Sequence 145, Application US/10452024
Sequence 145, Application US/10452024
Sequence 145, Application World Sequence 145, Application World Sequence 145, Application World Sequence 145, Application Sequence 145, Application Sequence 145, Applicant Sequence 145, Applicant Sequence 145, Applicant Sequence 145, Applicant Sequence 145, Application Number: US/10/452,024
CURRENT FILING DATE: 2002-06-02
PRIOR FILING DATE: 2002-06-31
NUMBER OF SEQ ID NOS: 188
SOFTWARE: Patentin version 3.2
SEQ ID NO 145
LENGTH: 1315
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Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0;
                                                                                                 US-10-241-259-141
) Sequence 141, Application US/10241596
) Publication No. US20030166238A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Microbiological Research Authority
APPLICANT: The Sperwood Laboratory Limited
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.013003
CURRENT APPLICATION NUMBER: US/10/241,596
CURRENT FILING DATE: 2002-09-12
PRIOR PELING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR PELING DATE: 1999-02-23
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Pred. No. 1.4e-05;
; Mismatches 0;
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; ORGANISM: Clostridium tetani
US-10-452-024-145
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; ORGANISM: Clostridium tetani
US-10-241-596-141
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US-09-848-834A-15
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US-10-452-024-145
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US-10-452-024-149
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LENGTH: 887
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100.0%; Score 79; DB 14; Length 879;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels C
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Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels
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US-10-241-596-143

US-10-241-596-143

GENERAL INPORMATION:

APPLICANT: MICROBIOLOGICAL Research Authority
APPLICANT: MICROBIOLOGICAL RESEARCH LIMITED

TILLE OF INVENTION: Recombinant Toxin Fragments
FILE REPRENCE: 1581.013003

CURRENT FILING DATE: 202-09-12

PRIOR PELLING DATE: 1999-02-23

PRIOR FILING DATE: 1999-02-23

PRIOR PELLING DATE: 1999-02-23

PRIOR PELLOATION NUMBER: US 09/242,689

PRIOR PELLOATION NUMBER: US 08/782,893

PRIOR PELLOATION NUMBER: US 08/782,893

PRIOR PELLOATION NUMBER: US 08/782,893

PRIOR FILING DATE: 1996-12-27

PRIOR FILING DATE: 1996-12-27

PRIOR FILING DATE: 1996-12-27

PRIOR FILING DATE: 1996-12-27

PRIOR FILING DATE: 1996-12-3

PRIOR FILING DATE: 1996-12-3

PRIOR FILING DATE: 1996-12-3

NUMBER OF SEQ ID NOS: 175

SEQ ID NO 143

LENGTH: 879
  APPLICANT: Microbiological Research Authority
APPLICANT: The Speywood Laboratory Limited
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.013003
CURRENT APPLICATION NUMBER: US/10/241,596
CURRENT PILING DATE: 2002-09-12
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR FILING DATE: 1999-02-23
PRIOR PILING DATE: 1996-02-23
PRIOR APPLICATION NUMBER: US 08/782,893
PRIOR PILING DATE: 1996-12-27
PRIOR PILING DATE: 1996-12-27
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR PILING DATE: 1996-12-13
PRIOR PILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: GB 9617671.4
PRIOR PILING DATE: 1996-08-23
NUMBER OF SEQ ID NOS: 175
SEQ ID NOS: 175
LENGTH: 872
LENGTH: 872
Microbiological Research Authority
The Speywood Laboratory Limited
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US-10-241-596-143
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; ORGANISM: Clostridium tetani
US-10-241-596-145
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US-10-452-024-149

US-10-452-024-149

Fequence 149, Application US/10452024

Fublication No. US20040013687A1

Fublication No. US20040013687A1

Fublication No. US20040013687A1

APPLICANT: Simpson, Lance

APPLICANT: Maksymowych, Andrew

TITLE OF INVENTION: Compositions and Methods For Transepithelial Molecular Transport

FILE REPERBICE: 1985-96U1

CURRENT FILING DATE: 2003-06-02

FRIOR PRILING DATE: 2003-06-02

PRIOR PRILING DATE: 2002-05-31

NUMBER OF SEQ ID NOS: 188

SOFTWARE Patentin version 3.2

SEQ ID NO 149

LENGHH: 1310
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100.0%; Score 79; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0;
US-10-241-590-14/
US-10-241-590-14/
US-10-241-590-14/
Publication No. US20030166238A1
GREAL INFOMATION:
APPLICANT: Microbiological Research Authority
APPLICANT: The Speywood Laboratory Limited
TITLE OF INVENTION: Recombinant Toxin Fragments
FILE REFERENCE: 1581.0130003
CURRENT APPLICATION NUMBER: US/10/241,596
CURRENT FILING DATE: 2002-09-12
PRIOR PELICATION NUMBER: US 09/25,829
PRIOR FILING DATE: 1999-02-23
PRIOR PLING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: US 09/242,689
PRIOR FILING DATE: 1999-02-23
PRIOR PLING DATE: 1999-02-23
PRIOR PLING DATE: 1996-02-24
PRIOR PLING DATE: 1996-12-27
PRIOR PLING DATE: 1996-12-27
PRIOR PLING DATE: 1996-12-27
PRIOR PLING DATE: 1996-12-13
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100.0%; Score 79; DB 14;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 16; Conservative 0; Mismatches 0;
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829 MOYIKANSKFIGITEL 844

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Sequence 177, Application US/10452024

Publication No. US20040013687A1

GENERAL INFORMATION:
APPLICAMT: Park, Jung-Beak
APPLICAMT: Park, Jung-Beak
APPLICAMT: Park, Jung-Beak
TITLE OF INVENTION: Compositions and Methods For Transepithelial Molecular TransporTITLE OF INVENTION NUMBER: US/10/452,024
CURRENT APPLICATION NUMBER: US/10/452,024
CURRENT PILING DATE: 2003-66-02
PRIOR PRILING DATE: 2003-06-0384,949
PRIOR FILING DATE: 2006-05-31
NUMBER OF SEQ ID NOS: 188
SOOTWARE: PatentIn version 3.2
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Best Local Similarity 100.0%; Pred. No. 5.4e-06; Matches 16; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1e-07;
iive 0; Mismatches 0;
                SOFTWARE ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/321,717
FILING DATE: 17-Dec-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PILING DATE: 40Known>
PILING DATE: 40Known>
PILING DATE: 40Known>
APPLICATION NUMBER: US 08/272,220
FILING DATE: 40Known>
REPLIATION NUMBER: US 08/272,220
ATTORNEY/AGENT INFORMATION:
NAME: DECONTI, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: DCI-092DV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-321-717-23
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-241-596-145; Sequence 145, Application US/10241596; Publication No. US20030166238A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08; Fr.
                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
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IYPE: amino acid
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; ORGANISM: Clostridium tetani
US-10-452-024-177
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Best Local Similarity 100.0
watches 16; Conservative
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                               APPLICANT: Hickey, William F.
Griffin, Ann C.
TITLE OF INVENTION: Proinsulin Peptide Compounds for Detecting and TITLE OF INVENTION: Treating Type I Diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Publication No. US20040002113A1
GENERAL INFORMATION:
APPLICANT: Griffin, Ann C.
Hickey, William F.
TILE OF INVENTION: Detection and Treatment Methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESS:
ADDRESSE: LAHIVE & COCKPIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER: READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEX-
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/346,563
FILING DATE: 16-Jan-2003
CLASSIPICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/472,704
FILING DATE: 06-JULY-1994
FILING DATE: 08-JULY-1994
                                                                                                                NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
REPERENCE/DOCKET NUMBER: DCI-092
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (617)227-7400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-346-563-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
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           GENERAL INFORMATION
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US-10-321-717-23
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sequence 2,

us-09-848-834a-2.open.rapb

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FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(16)
COTHER INFORMATION: Amino acid sequence 829-844 of the Tetanus
COTHER INFORMATION: Toxoid Precursor (Tentoxylysin)
US-09-848-8344-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 79; DB 9; Length 16; 100.0%; Pred. No. 9.5e-08; Live 0; Mismatches 0; Indels
     Sequence 2, Application US/09848834A;
Sequence 2, Application US/09848834A;
Patent No. US20020076416A1
GENERAL INFORMATION:
APPLICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOGTWARR: Patentin Version 3:0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-10-346-563-23
; Sequence 23, Application US/10346563
; Publication No. US20030220229A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOYIKANSKFIGITEL 16
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Best Local Similarity 100.
Matches 16; Conservative
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                                   US-09-848-834A-2
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Sequence 13, Appl
Sequence 145, Appl
Sequence 147, Appl
Sequence 147, Appl
Sequence 147, Appl
Sequence 141, Appl
Sequence 145, Appl
Sequence 15, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 9, Appli
Sequence 9, Appli
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                                                                               March 10, 2004, 09:16:59 ; Search time 12.5759 Seconds (without alignments) 268.645 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCCMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_MBW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-346-563-23
US-10-346-563-23
US-10-452-024-177
US-10-241-596-145
US-10-241-596-145
US-10-241-596-145
US-10-241-596-145
US-10-452-024-145
US-10-452-024-145
US-10-348-84A-15
US-09-848-84A-15
US-09-848-84A-15
US-10-339-522-9
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                                                                                                                                                                                                                                                                                                                                             Listing first 45 summaries
                                                            OM protein - protein search, using sw model
                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                              1 MOYIKANSKFIGITEL 16
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Match Length
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                                                                                                                                                   Perfect score:
                                                                                                                                                                 Sequence:
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Sequence 7, Appli Sequence 7, Appli Sequence 11, Appli Sequence 1, Appli Sequence 8, Appli Sequence 8, Appli Sequence 3, Appli Sequence 4, Appli Sequence 6, Appli

Sequence 14, Sequence 16,

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Sequence 4, Appli Sequence 1, Appli Sequence 7, Appli Sequence 13, Appli Sequence 13, Appli Sequence 19, Appli Sequence 618, Appli Sequence 7, Appli Sequence 64, Appli Sequence 145, Appli Sequence 175, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 619, Appli Sequence 5, Appli Sequence 620, Appli Sequence 620, Appli

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Caralle-Fup/Sp. and form Laporatory Strains.";

Caralle-Fup/Sp. Caralle-Sp. to the EmBL/GenBank/DDBJ databases.

Caralle-Fup/Sp. Caralle-Fup/Sp. 1;

Caralle-Fup/Sp. Caralle-Fup/Sp. 1;

Caralle-Fup/Sp. Caralle-Fup/Sp. 1;

Caralle-Fup/Sp. Caralle-Fup/Sp. 1;

Caralle-Fup/Sp. Caralle-Fup/Sp. 1;

Caralle-Fup/Sp. Caralle-Fup/Sp. 1;

Caralle-Fup/Sp. Caralle-Fup/Sp. 1;

Caralle-Fup/Sp. From Sp. 1;

Caralle-Fup/Sp. 1;

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NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.3%; Score 81; DB 5; Length 80; 89.5%; Pred. No. 3.5e-05; ive 0; Mismatches 2; Indels
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Job time : 20.7665 secs
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Best Local Si
Matches 17;
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Q9UOP6;
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Matches
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"Sequence variation in the non-repeat region of the Plasmodium
"Sequence variation in the non-repeat region of the Plasmodium
lanciparum glutamate rich protein (GLUPP) from Brazil, Senegalese, and
Burnese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJZ69941; CAB64167.1;
CAP6107373; RAGEGRS-/Immunity protein activity; IEA.
InterPro; IPR003067; Cromsprzoite.
InterPro; IPR003067; Cromsprzoite.
FEAM; PF00090; tsp_1; 1.
PFAMET; SM01209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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GO; GO:0003793; F:defense/immunity protein activity; IEA.
                                     InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000804; TSP1.
Pfam; PF00090; LSP_1. 1.
SMRTS; PR01303; CRCMSPRZOITE.
SMRT; SM00209; TSP1; 1.
NON_TER 1 1 1.
NON_TER 80 80 80
SEQÜENCE 80 AA; 9043 MW; 17282E319AE508B3 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Circumsporozoite protein (Fragment).
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Circumsporozoite protein (Fragment).
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Best Local Similarity 89.5'
Matches 17, Conservative
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Q9U0Q4;
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de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

The Sequence variation in the non-repeat region of the Plasmodium of a Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Stricker Str
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STRAIN=PALO ALTO, and D50;

GA STRICKER K., Vuset J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuset J., Jepsen S., Oeuvray C., Theisen M.;

Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ269954; CAB64179.1;

EMBL; AJ269944; CAB64170.1;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
//CBI_TaxID=5833;
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NCBI_TaxID=5833;
                       Length 80;
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Pred. No. 3.5e-05,
0; Mismatches 2; Indels
                                                                                     2; Indels
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(Tremblrel. 13, Last sequence update)
(Tremblrel. 24, Last annotation update)
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                       85.3%; Score 81; DB 5; 1
89.5%; Pred. No. 3.5e-05;
                                                                                     0; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Matches 17; Conservative
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NCBL_TaxID=5833;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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Pred. No. 3.5e-05;
0; Mismatches 2; Indels
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                                                                                            Last sequence update)
Last annotation update)
                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
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Pfam; PF00090; tsp 1; 1.
PRINTS; PR01130; CREMSPRZOITE.
SMART; SM0209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
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ilarity 89.5%;
Conservative 0
PRELIMINARY;
                                                                                                                                                                                                                Plasmodium falciparum.
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GENERAL FROM N.T.

STRAIN=11;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and

falciparum glutamate rich protein (GLURP) from Brazil, Senegalese,

Burmese field isolates and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ26991; CAB64176.1;

BMBL, AJ26991; CAB64176.1;

RML; FROMO3097; Franchimmunity protein activity; IEA.

BROW GOORD (SEP-1999) TSPI. 1.

RRINTS: PRO1303; CRCWSPRZOITE.

SMART; SMO0209; TSPI. 1.

PROSTITE, PSS0092; TSPI. 1.

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de Stricker K., Vunst J., Jepsen S., Oeuvray C., Theisen M.;

de Stricker K., Vunst J., Jepsen S., Oeuvray C., Theisen M.;

The sequence variation in the non-repeat region of the Plasmodium.

The sequence variation in the non-repeat region of the Plasmodium.

The sequence variation in the non-repeat region of the Plasmodium.

The sequence variation in the non-repeat region of the Plasmodium.

The sequence variation in the sequence and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ269964; CAB64183.1; -.

REMBL; AJ269964; CAB64183.1; -.

GO; GO:000793; Fedense/immunity protein activity; IEA.

RICHERPO; IPR000884; TSP1.

RICHERPO; IPR000909; LSP1.

REMBL; PR01303; CRCMSPRZOITE.

REMBL; PR01303; CRCMSPRZOITE.
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Best Local Similarity 89.5%; Pred. No. 3.5e-05;
Matches 17; Conservative 0; Mismatches 2; Indels
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89.5%; Pred. No. 3.5e-05;
iive 0; Mismatches 2; Indels
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2003 (TrEMBLrel. 24, Last annotation update)
Circumsporozoite protein (Fragment).
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"Conservation and heterogeneity of the glutamate-rich protein (GLURP)
among field isolates and laboratory lines of Plasmodium falciparum.";
Mol. Biochem. Parasitol. 111:123-130(2000).
EMBL; AJ269978; CAB64197.1;
GG; GG:0003793; Fedefense/immunity protein activity; IEA.
InterPro; IPR003067; Cremsprzoite.
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Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Best Local Similarity 89.5%; Pred. No. 3.5e-05;
Matches 17; Conservative 0; Mismatches 2; Indels
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Best Local Similarity 89.5%; Pred. No. 3.5e-05;
Matches 17; Conservative 0; Mismatches 2; Indels
    GO; GO:0003793; F:defense/immunity protein activity; IEA.
InterPro; IPR003067; Cromsprzoite.
InterPro; IPR00884; TSP1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSRZOITE.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
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SMART; SM00209; TSP1; 1.
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SEQÜENCE 80 AA; 9102 MW; BFC6C970CEF0PA3E CRC64;
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SEQUENCE 80 AA; 9000 MW; 036C7E319AFE13B3 CRC64;
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01-VAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Circumsporozoite protein (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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STRAIN=B1896;
MEDLINE=20542035; PubMed=11087922;
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Q9UOP1,
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STRAINMI1, and D7;

GESTICKER K., Vules J., Jepsen S., Oeuvray C., Theisen M.;

Sequence variation in the non-repeat region of the plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
falciparum glutamate rich protein Brazil, Senegalese, and
falciparum glutamate rich protein GLURP) from Brazil, Senegalese, and
BNBL; AJ269947, CAB64122.1;

GO; GO:O003793; F.Gefense/limmunity protein activity; IEA.
InterPro; IPR000864; TSP1.
                                                                                                                                                                                                                                                                                                                                      de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
"Sequence variation in the non-repeat region of the Plasmodium
"Sequence variation in the non-repeat region of the Plasmodium
falcipatum glutamate rich protein (GLDNE) from Brazil, Senegalese, and
Burmese field isolaters and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269965; CAB64188.1; -.
EMBL; AJ269965; CAB64188.1; -.
InterPro; IPR000864; TSP1.
InterPro; IPR000864; TSP1.
Pfam; PP00090; tsp_1; 1.
PRINTS; PR01303; CECKSPRZOITE.
SMART; SM00209; TSP1:
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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VCBI_TaxID=5833;
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80 AA; 9123 MW; 4614EEC68F0B1434 CRC64;
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SEQUENCE 80 AA; 9033 MW; BA71EBE0DB03193B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Circumsprozoite protein (Fragment).
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PFam; PP00090; tsp_1; 1.
PRINTS, PR01303; CRCMSPRZOITE.
SWART; SMO0209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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STRAIN=D4405;
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STRAIN=D4403, and D4259;
STRAIN=D4403, and D4259;
GFRAIN=D4403, and D4259;
GFRAIN=D4403, and D4259;
GFRAIN=D403, and D4259;
Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269962; CAB64187.1;
EMBL; AJ269962; CAB64181.1;
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STRAIN-D4230;

STRAIN-D4230;

G SEXTERIN-D4230;

G SETAIN-D4230;

G SETAIN-D4230;

"Sequence variation in the non-repeat region of the Plasmodium
"Sequence variation in the non-repeat region of the Plasmodium
falciparum glutamate rich protein (GLMP) from Brazil, Senegalese, and
Burmese field isolates and from laboratory strains.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJZ69961; CAB64180.1;

EMBL; AJZ69961; CAB64180.1;

EMBL; CAB64180.1;

InterPro; IPR003067; Cremsprzoite.
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5833;
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Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
VOBI_TaxID=5833;
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89.5%; Pred. No. 3.5e-05;
tive 0; Mismatches 2; Indels
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Score 81; DB 5; I
Pred. No. 3.5e-05;
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                                                                                                               2 EKKIAKMEKASSVFNVVNS 20
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
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        Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Circumsporozoite protein II (Fragment).
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Cyaccesion: 151092
Ry Lungland, H.; Lorens, J.B.; Andersen, O.; Kisen, G.O.; Alestrom, P.
Ry Lungland, H.; Lorens, J.B.; Andersen, O.; Kisen, G.O.; Alestrom, P.
Ry Lile: The Atlantic salmon prepro-gonadotropin releasing hormone gene and mRNA.
A; Reference number: 151040; MUID:92267241; PMID:1587389
A; Accession: 151092
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-74 < KLU3
A; Cross-references: EMBL:X79711; NID:9499322; PID:9499323
                                                                           C; Accession: A21114
R; Sherwood, N.; Eiden, L.; Brownstein, M.; Spiess, J.; Rivier, J.; Vale, W. Proc. Natl. Acad. Sci. U.S.A. 80, 2794-2798, 1983
A; Title: Characterization of a teleost gonadotropin-releasing hormone.
A; Reference number: A21114; MUID: 83195140; PMID: 6341999
A; Accession: A21114
A; Stetus: preliminary
A; Molecule type: protein
A; Residues: 1-10 SSHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gonadotropin releasing hormone - chinook salmon (fragment)
C/Species: Oncorhynchus tschawytscha (chinook salmon)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Aug-1997
gonadoliberin - chum salmon
C;Species: Oncorhynchus keta (chum salmon)
C;Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 18-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                72.2%; Score 39; DB 2; Length 10; 75.0%; Pred. No. 0.33; 2; Indels tive 0; Mismatches 2; Indels
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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A,Gene: GnRH
A;Introns: 38/3; 65/3
gonadoliberin
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Search completed: March 10, 2004, 09:16:38 Job time: 4.17166 secs

17 HWSYGWLP 24

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A, Molecule type: protein
A, Molecule type: protein
A; Residues: 22-31 < 8033-3
A; Residues: 22-31 < 8033-3
A; Residues: 22-31 < 8033-3
A; Residues: 22-31 < 8033-3
C; Superfamily: gonadoliberin
C; Superfamily: gonadoliberin i #status predicted <813-8
F; 22-31/Product: gonadoliberin I #status experimental <MATI>
F; 25-80/Product: gonadoliberin I - associated protein #status predicted <MATI>
F; 22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime
F; 22/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roles as a hypophysictropic factor, and a physiologic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Rosidues: 1.46,'S',48-59,'G',61-80 <BOG2>
A;Rosidues: 1.46,'S',48-59,'G',61-80 <BOG2>
A;Cross-references: EMBL:X78048; NID:9459431; PIDN:CAA54970.1; PID:9459432
A;Cross-references: EMBL:X78048; NID:9459431; PIDN:CAA54970.1; PID:9459432
A;Note: gonadoliberin 1.associated protein form II, presumed to be a polymorphic form R;Bogerd, J:, Li, K.W.; Janssen-Domerholt, C.; Goos, H.
Biochem. Biophys. Res. Commun. 187, 127-134, 1992
A;Title: Two gonadotropin-releasing hormones from African catfish (Clarias gariepinus). A;Reference number: JC1242; MUID:92392313; PMID:1520292
                                                                                  NyAltermate names: gonadoliberin, catfish-type; gonadotropin-releasing hormone I (GnRH) NyAltermate names: gonadoliberin, catfish-type; gonadoriberin I; gonadoliberin I; species: Glarias gariepinus (sharptoch catfish) C; paccession: S45601, 3C1242; S42936; S42937 #text_change 18-Jun-1999 C; Accession: S45602; S45601; JC1242; S42936; S42937 #text_change I8-Jun-1999 Bur. J. Bandbergen, T.; Andersson, B.; Goos, H. Bur. D. Biochem: 222, 541-549, 1994 A; fitle: Isolation, characterization and expression of cDNAs encoding the catfish-type A; Reference number: S45600; MUID:94291651; PMID:8020492
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A;Molecule type: mRNA
A;Residues: 1.80 <BOG1>
A;Residues: 1.80 <BOG1>
A;Residues: 1.80 <BOG1>
A;Residues: I.80 <BOG1>
A;Residues: I.80 <BOG1>
A;Residues: I.80 <BOG1>
A;Residues: Bobb:X78049; NID:g459433; PIDN:CAA54971.1; PID:g459434
A;Note: gonadoliberin I-associated protein form I
A;Accession: S45601
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Pred. No. 1.1;
1; Mismatches

    sharptooth catfish

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A,Molecule type: mRNA
A,Residues: 1-91 < OKUJ-
A,Cross-references: DDBJ:AB041333
C,Comment: This protein plays the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h
Similarity 75.0%;
6; Conservative 1
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C;Superfamily: gonadoliberin
C;Keywords: brain
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23 HWSHGLNP 30
                                                                        gonadoliberin I precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 HWSYGLRP 9
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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A, Accession: B53561
A, Accession: B53561
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-374 exury
A, Molecule type: DNA
A, Residues: 1-374 exury
A, Residues: 1-374 exury
A, Residues: 1-374 exury
A, Residues: 1-374 exury
A, Residues: 1-374 exury
A, Residues: 1-374 exury
A, Residues: 1-374 exury
A, Experimental source: strain 1021, megaplasmid pSymA abola, P.; Ampe, F.; Barloy-Hubler, R, Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler, B, Hyman, R.W.; Jones, T.M.; Long, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.A; Reference number: A96039; MUID:21368234; PMID:11474104
A, Contents: annotation
C, Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: E95361
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
R;Ralman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 9813-9889, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilod
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                             gonadotropin-releasing hormone - Cichlid (Haplochromis burtoni)
C;Species: Haplochromis burtoni
C;Date: 13.5ep-1996 #sequence_revision 13.5ep-1996 #text_change 21-Jul-2000
C;Date: 150739
C;Accession: 150739
R;White, S.A.; Kasten, T.L.; Bond, C.T.; Adelman, J.P.; Fernald, R.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 8363-8367, 1995
A;Title: Three gonadotropin-releasing hormone genes in one organism suggest novel roles A;Reference number: 150739; MUID:95396797; PMID:7667296
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    Sinorhizobium meliloti

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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U31865; NID:g905398; PIDN:AAC59691.1; PID:g905399
C;Superfamily: gonadoliberin
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                         Gaps
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                            Indels
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Pred. No. 3.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-98 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
Pred. No. 0.088;
L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB 2;
Pred. No. 0.22;
0; Mismatches
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A;Genome: plasmid
C;Keywords: intramolecular lyase; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.6%;
Similarity 85.7%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.2%;
ilarity 87.5%;
Conservative
   87.5%;
   Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity
7; Conserve
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                                                                                                                                              HWSYGLOP 32
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                                                                                     2 HWSYGLRP 9
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Best Local Similarity
Matches 6; Conserv
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RESULT 8

RHAQ1

Sonadoliberin I - American alligator
NyAlternate names: gonadotropin-releasing hormone I
Sybecies: Alligator mississippiensis (American alligator)
C;Species: Alligator mississippiensis (American alligator)
C;Species: Alligator mississippiensis (American alligator)
C;Species: J. Mar-1993 #sequence_revision 31-Mar-1993 #text_change 18-Mar-1997
C;Accession: A60066
R;Loveioy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swansc Regul. Pept. 33, 105-116, 1991
A;Title: Primary structure of two forms of gonadotropin-releasing hormone from brains of A;Reference number: A60066; MUID:91352338; PMID:1882082
                                                                                                                                                          A, Description: stimulates pituitary secretion of lutropin and follitropin
A; Note: gonadoliberin-associated protein may have prolactin release inhibiting activiy
A; Note: gonadoliberin-associated protein may have prolactin release inhibiting activiy
C; Superfamily: gonadoliberin
C; Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid;
F; 1-23/Domain: signal sequence #status predicted <SIGN>
F; 24-32/Product: progonadoliberin #status predicted <GIN>
F; 24-32/Product: prolactin release-inhibiting factor #status predicted <PIF>
F; 24/Modified site: pyrrolidone carboxylic acid (GIN) (in mature form) #status predicts
F; 33/Modified site: amidated carboxyl end (GIy) (amide in mature form from following g]
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NyAlternate names: gonadotropin-releasing hormone I
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cipate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
CiAccession: ISO644; S33507
Ribum, I.C.; Chen, Y.; Hock, C.; Sharp, P.J.; Sang, H.M.
J. Mol. Endocrinol. 11, 19-29, 1993 Hormone Preprogonadotrophin-releasing hormone-I gene.
A; Reference number: ISO644; MUID:94059355; PMID:7902095
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A;Cross-references: EMBL:X69491; NID:g496326; PIDN:CAA49246.1; PID:g311612
sequence extracted from NCBI backbone (NCBIN:121082, NCBIP:121083)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Residues: 1-10 <LOV>
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end, hormone, hypothalamus, pyroglutamic ac:
E;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;1/Modified site: amidated carboxyl end (Gly) #status experimental
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Pred. No. 0.0077;
1; Mismatches 0; Indels
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0; Mismatches
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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Best Local Similarity 87.5
Matches 7; Conservative
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Matches 8; Conservative
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A,Introns: 47/3; 79/3
C;Superfamily: gonadoliberin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HWSYGLRP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 HWSYGLRP 9
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                                                                                              A; Introns: 47/3;
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                                                                C;Genetics:
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NyAlternate names: gonadoliberin-associated protein (GAP); gonadotropin releasing hormon

NyAlternate names: gonadoliberin-associated protein (GAP); gonadotropin releasing hormon

NyContains: gonadoliberin; prolactin release-inhibiting factor

CyBecies: Rattus norregicus (Norway rat)

CyBecies: Rattus norregicus (Norway rat)

CyBecies: Amar-1988 #sequence revision 31-Mar-1988 #text_change 18-Jun-1999

CyBecies: Anar-1988 #sequence revision 31-Mar-1988 #text_change 18-Jun-1999

RyBond, C.T.; Hayfilck, J.S.; Seeburg, P.H.; Adelman, J.P.

Mol. Endocrinol. 3, 1257-1262, 1989

Ayfilce: The rat gonadotropin-releasing hormone: SH locus: structure and hypothalamic ex

AyReference number: A40147; MUID:89384661; PMID:2476669
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A, Residues: 1-92 - SBON>

A, Fereidues: 1-92 - SBON>

A, Cross-references: GB: M31670, NID: 9204447; PIDN: AA41264.1; PID: 9204448

R; Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Seeburg, P.H.

R; Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Seeburg, P.H.

B, Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Seeburg, P.H.

A; Title: Isolation of the gene and hypothalamic cDNA for the common precursor of gonador

A; Reference number: A94090; MUID: 86094338; PMID: 2867548
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A,Molecule type: mRNA
A,Molecule type: mRNA
A,Fosidues: 1-92 ADB3
A,Cross-references: GB M12579, NID:g204445, PIDN:AAA41263.1; PID:g204446
A,Cross-references: GB M2579, NID:g204445, PIDN:AAA41263.1; PID:g204446
R;Maler, C.C.; Marchetti, B.; LeBoeuf, R.D.; Blalock, J.E.
C.G.; Marchetti, B.; LeBoeuf, R.D.; Blalock, J.E.
A;Title: Thymocytes express a mRNA that is identical to hypothalamic luteinizing hormone
A;Reference number: A48410; MUID:93105480; PMID:1468115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Ceross-references: GDB:133746; OMIM:227200; OMIM:152760
A;Map position: 8p21-8p11.2
A;Map position: 8p21-8p11.2
A;Map position: 47/3; 79/3
C;Function: 47/3; 79/3
C;Function: gonadoliberin stimulates pituitary secretion of lutropin and follitropin A;Doscription: gonadoliberin associated protein may have prolactin release inhibiting activiy C;Superfamily: gonadoliberin essociated protein may have prolactin release inhibiting activiy C;Superfamily: gonadoliberin effects predicted (SIG)
F;1-23/Domain: signal sequence ffstatus predicted (SIG)
F;2-92/Product: gonadoliberin #status predicted (SIG)
F;2-92/Product: gonadoliberin #status experimental (MAT)
F;2-92/Product: gonadoliberin-associated protein #status fredicted (GAP)
F;2-4-33/Product: gonadoliberin-associated protein #status fredicted (GAP)
F;2-4-33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen F;3-4-33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly
                                                                                                                                                                                   A Accession: A90108
A) Molecule type: protein
A) Molecule: 24-33 < TAN>
A) Experimental source: placental trophoblasts
A) Experimental source: placental trophoblasts
B) Elebbovitz, D; Koch, Y; Pitzer, F; Fridkin, M.; Dantes, A.; Baumeister, W.; Amsterda Fibs. Lett. 346, 203-206, 1994
A) Title: Sequential degradation of the neuropeptide gonadotropin-releasing hormone by th A) Contents: annotation; degradation pathway of synthetic hormone
C)Genetics:
                     R;Tan, L.; Rousseau, P.
Blochem: Biophys. Res.
A;Title: The chemical identity of the immunoreactive LHRH-like peptide biosynthesized
A;Reference number: A90108; MUID:83126573; PMID:6760865
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A;Residues: 1-2 <NMI>
A;Cross-references: GB:S50870; NID:g262059; PIDN:AAB24572.1; PID:g262060
A;Experimental source: thymus
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Les 8; Conservative
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A; Status: pre
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Nyllermeterin precurer, variable unitality of National Nyllermiterin precurer, releasing Nyllermete names: gonadotroplaria releasing hormone (GnRH); luteinizing hormone releasing Nyllermete names: gonadotroplaria protein (GAP); progonadoliberin (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo source) (Species: Homo sapiens (man) (Species: Homo source) (Species: Homo source) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) (Species: Natural) 
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A;Molecule type: mRNA
A;Residues: 1-92 (ADDS:
A;Cross-references: GB:ML2578; NID:g183418; PIDN:AAA35916.1; PID:g386749
A;Cross-references: GB:ML2578; NID:g183418; PIDN:AAA35916.1; PID:g386749
A;Cross-references: Dypothalamus
R;Seeburg, P.H.; Adelman, J.P.
Nature: 311, 666-668, 1984
A;Title: Characterization of cDNA for precursor of human luteinizing hormone releasing
A;Reference number: A93342; MUID:85012739; PMID:6090951
                                                                                                                                                                                                                                                  CiAccession: A47578
KiMason, A.J.; Hayflick, J.S.; Zoeller, R.T.; Young III, W.S.; Phillips, H.S.; Nikolice Science 234, 1366-1371, 1986
A;Title: A deletion truncating the gonadotropin-releasing hormone gene is responsible f A;Reference number: A47878; MUID:87069928; PMID:3024317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gonadoliberin precursor - mouse
NiAlternate names: gonadotrophir-releasing hormone (GnRH); luteinizing hormone
NiContains gonadoliberin; gonadoliberin-associated protein (GAP)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 18-Mar-1997 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: DNA
A,Residues: 1-90 <MAS>
A,Cross-references: EMBL:M14872; NID:g193576; PIDN:AAA37717.1; PID:g387175
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A,Resdudes: 1-15,'8', 17-92 <SEE>
A,Cross-references: GB:X01059; NID:g34356; PIDN:CAA25526.1; PID:g34357
A,Experimental source: placenta
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Pred, No. 0.016;
0; Mismatches 0; Indels
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/ 100.0%; Pred. No. v.
'... 0; Mismatches
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Best Local Similarity
Matches 8; Conserv
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Nathernate names: lucahiaing hormone releasing hormone
C;Species: Macaca mulatta (friesus macaque)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
R;Aaccention: 1984
Neuroendocrinology 60, 346-159, 1994
Neuroendocrinology 60, 346-159, 1994
A;Atitle: Developmental expression of the genes encoding transforming growth factor alpha
A;Reference number: 158344
A;Accession: 178541
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N.Alternate names: luteinizing hormone releasing hormone
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13.5ep-1996 #sequence_revision 13.5ep-1996 #text_change 16-Jul-1999
C;Accession: 151423
R;Hayes, W.P.; Wray, S.; Battey, J.F.
Endocrinology 134, 1835-1845, 1994
A;Title: The frog GnRH-I gene has a mammalian-like expression pattern and conserved doma A;Reference number: 151423; MUID:94185563; PMID:8137750
A, Residues: 1-10 cBUR>

A, Note: the natural and synthetic hormones have the same biological activity
C, Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and for Superfamily: gonadoliberin
C, Superfamily: gonadoliberin
C, Superfamily: stronglutamic acid
F, 1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F, 10/Modified site: amidated carboxyl end (Gly) #status experimental
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Nolecule type: DNA
A,Rosidues: 1-89 <HAY>
A,Cross-references: GB:L28040; NID:g496291; PIDN:AAA49728.1; PID:g496292
C,Genetics:
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A;Molecule type: mENA
A;Molecule type: mENA
A;Residues: 1-7 < RES2
A;Cross-references: GB:S75918; NID:g912831; PIDN:AAB33096.1; PID:g912832
C;Superfamily: gonadoliberin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.3%; Score 52; DB 2; Length 89;
100.0%; Pred. No. 0.016;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                 96.3%; Score 52; DB 1; Length 10; 100.0%; Pred. No. 0.0015; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity luve
And 8; Conservative
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C,Superfamily: gonadoliberin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HWSYGLRP 32
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Best Local Similarity
Matches 8; Conserv
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March 10, 2004, 08:58:54 ; Search time 3.11284 Seconds (without alignments) 309.015 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                       283366 segs, 96191526 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                   US-09-848-834A-1
54
1 XHWSYGLRPX 10
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1: Dirl:*
2: Dir2:*
3: Dir3:*
4: pir4:*
                                                                                                                                                                                       Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	gonadoliberin - pi		gonadoliberin prec	gonadoliberin prec					gonadoliberin I pr	gonadotropin-relea	probable muconate	gonadoliberin I pr	medaka-type gonado	gonadoliberin - ch	gonadotropin relea	gonadotropin-relea	gonadotropin relea	gonadotropin-relea	gonadotropin relea	salmon-type gonado	gonadoliberin prec	gonadoliberin pred	probable fmu prote	831B				7.10	hypothetical 345 p
SUMMARIES	ΩI		RHSHG			RHMSG	RHHUG													151331					T1885	D8447	G1269	T3284	F1	A5851
	DB		Н	0	Ŋ	-	٦	Н	-	N	Ŋ	Ŋ	Н	N	7	N	N	N	Ŋ	N	~	N	71	~	~	N	7	N	71	N
	Length	10	10	67	89	90	92	92	10	92	98	374	80	91	10	74	82	82	8	82	06	96	90	w	A.	w	O,	$\overline{}$	270	4.
de	Query	96.3	96.3	96.3	96.3	96.3	96.3	96.3		88.9															72.2	70.4	70.4	70.4	68.5	68.5
	Score	. ເນ	52	52	52	52	52	52	48	48	46	43	42	42	99	39	39	39	39	99	8	8	9	39	39	38	38	38	37	37
	Result No.	1	C)	m	4	'n	v	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

gonadoliberin - sheep
Gonadoliberin - sheep
Gispecies: Ovis crientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
Cispecies: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Mar-1997
Ciscession: A93780; A01411
Ciscession: A3780; A01411
Proc. Natl. Acad. Sd: U.S.A. 69, 278-282, 1972
A;Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing fact A;Reference number: A33780; MUID:72094314; PMID:4550508
A;Molecule type: protein

RESULT 2

RHSHG

hypothetical prote hypothetical prote protein C13A10.3 [hypothetical prote hypothetical prote stage V sporulatio	conserved hypothet peptidase, M16 fam	hypothetical prote inorganic pyrophos	nypotnetical proce aldose reductase h ylil protein precu	probable dehydroge probable dehydroge probable oxidoredu
	2 E95323 2 T27432 2 D96971			2 D64696 2 A53440 1 E64821	2 B90743 2 A85594 2 AB0604
	66.7 327			64.8 308 64.8 316 64.8 371	64.8 371 64.8 371 64.8 373
	. w w w				3333
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ALIGNMENTS

RESULT 1 RHSGLT 1 RHSGLT 1 RHSGL 2000 C10 C10 C10 C10 C10 C10 C10 C10 C10	18-Mar-1997 . II. Confirmation of the solid-phase methorhemical and biological ing hormone. It both luteinizing and for the solid sperimental sental 0; Gaps 0;
Oy 2 HWSYGLRP 9	

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The proposed amino acid
                                                                                                                                                                        96.3%; Score 52; DB 1; Length 10; 100.0%; Pred. No. 0.0025; tive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                   US-08-343-883-1
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Search completed: March 10, 2004, 09:28:50 Job time : 4.8716 secs

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Gaps , 0

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Sequence 1, Application US/08343883
Sequence 1, Application US/08343883
Sequence 1, Application US/08343883
Setent No. 5573767
GENERAL INFORMATION:
APPLICANT: Dollout, Claude J.M.
APPLICANT: Chouvet, Claire D.
APPLICANT: Chouvet, Claire D.
TITLE OF INVENTION: Method for improving the organoleptic
TITLE OF INVENTION: qualities of the meat from uncastrated male domestic
TITLE OF INVENTION: animals, vaccines which are usable in this method, ne
TITLE OF INVENTION: peptide, in particular for producing these vaccines.
NUMBER OF SEQUENCES: 2
                                                                                              RESULT 14

US-08-184-935-6

I Sequence 6, Application US/08184935

Patent No. 5476770

GENERAL INFORMATION:

APPLICANT: PRADELLES, PHILIPPE

TITLE OF INVENTION: OR HAPTEN

TITLE OF INVENTION: OR HAPTEN

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, STAME: VITINGTON

STAME: VITINGTON

STAME: VITINGTON

CITY: Arington

STAME: VITINGTON

COMPUTER: US.A.

ZIP: 22202

COMPUTER: US.A.

ZIP: 22202

COMPUTER: Ploppy disk

COMPUTER: Ploppy disk

COMPUTER: PRADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/184,935

FILING DATE: 24-JAN-1994

CLASSIFICATION NUMBER: 24-JAN-1994

CLASSIFICATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 24,618

TELECHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.3%; Score 52; DB 1; Length 10; 100.0%; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 10 OTHER INFORMATION: /note= "C-terminal amide" US-08-184-935-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEX: 248855 09AT UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 10 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
LOCATION: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 HWSYGLRP 9
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Best Local Similarity
Matches 8; Conserv
US-08-343-883-1
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JAPLICANT: FU LU, Mou-Ying
APPLICANT: Subba Rao, Gowdahallin N.
APPLICANT: Lee, Dennis G.
TITLE OF INVENTION: Pormulations and Method for the
TITLE OF INVENTION: Percutaneous Administration of Leuprolide
TITLE OF INVENTION: Percutaneous Administration of Leuprolide
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Dept. 377 Abbott Laboratories
STREET: One Abbott Park
STREET: One Abbott Park
CITY: Abbott Park
STREET: One Abbott Park
STREET: One Abbott Park
COMPUTER: ILL
COUNTRY: USA
ILL
COMPUTER: IBM PC Compatible
ORMUTER: IBM PC COMPATA: S141
ATTORNEY/AGENT INFORMATION:
NAME: Janssen, Jetry P.
REGISTRATION NUMBER: 29,175
REGISTRATION NUMBER: 29,175
REGISTRATION NUMBER: 29,175
REGISTRATION NUMBER: 29,175
REGISTRATION NUMBER: S165.US.OI
TELEPHONE: (708) 937-956
INPORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
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96.3%; Score 52; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0025;
Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                              Query Match 96.3%; Score 52; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0025; Matches 8; Conservative 0; Mismatches 0; Indels
                                   1 LOCATION: 1
7 OTHER INFORMATION: /note= "Xaa at position 1 is a
7 OTHER INFORMATION: 5-0xo-prolyl aminoacyl residue."
US-08-103-022-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /note= "XAA at position 10 is
OTHER INFORMATION: glycyl-amide residue"
US-07-897-680-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "XAA at position 1 is pyro-glutamyl residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/07897680
Patent No. 5446025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10 anino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note
OTHER INFORMATION: pyro-
           NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                              2 HWSYGLRP 9
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Indels

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Gaps

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haviv, Fortuna
APPLICANT: Fitzpatrick, Timothy D.
APPLICANT: Fitzpatrick, Timothy D.
APPLICANT: Nichols, Charles J.
APPLICANT: Mort, Nichols G.
APPLICANT: Mort, Nichols A.
APPLICANT: Mort, Nichols A.
APPLICANT: Mort, Nichols A.
APPLICANT: Mort, Nichols A.
APPLICANT: Mort, Nichols A.
APPLICANT: Mort, Nichols A.
ADDRESSE: Edward H. Gorman, Jr., Dept. 377
STREET: Abott Laboratories, One Abbott Park Road
CITY: No. 5413990th Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: FIGURY CLEAR
COMPUTER: IN FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURFWARE: Patentin Release #1.0, Version #1.25
SURFWARE: Patentin Release #1.0, Version #1.25
SURFWARE: Datentin Release #1.0, Version #1.25
TLING DATE: 05-OCT-1993
CLASSIFICATION NUMBER: US-07
ATTORNEY/AGENT INFORMATION:
NAME: Jansen, Jerry F.
REGISTRATION NUMBER: 5389.US.O1
TELEPRATION NUMBER: 5389.US.O1
TELEPRATION NUMBER: 5389.US.O1
TELEPRATION NUMBER: 5389.US.O1
TELEPRAX: (708) 938-7742
TELEPRAX: (708) 938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHRACTERISTICS:
SEQUENCE CHRACTERISTICS:
                                                                             FILING DATE: 25-UJN-1991
CLASSIFICATION 435
PRIOR APPLICATION DATE: 435
PRIOR APPLICATION DATE: PCT/AU90/00373
FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/148 CHAC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amin acide
                                                                  US/07/690,983D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08103022
Patent No. 5413990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HWSYGLRP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 HWSYGLRP 9
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STRANDEDNESS: si
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US-07-690-983D-32
Sequence 32, Application US/07690983D
Patent No. 5403586
GENERAL INFORMATION:
MAPPLICANT: STEWART, Andrew G.
APPLICANT: STEWART, Andrew G.
APPLICANT: TSONIS, Con G.
TITLE OF INVENTION:
CORRESSED ADDRESS:
ADDRESSEDS: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: Washington, D.C.
COUNTRY: BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: TatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,983D
FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: PCT/AU90/00373
FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
ARGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/148 CHAC
TELEFRAN: (202)672-5300
TTELEFRAX: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 37, Application US/07690993D; Patent No. 540386; GENBEAL INFORMATION:
APPLICANT: RUSSELL-JONES, Gregory J. APPLICANT: STEWART, Andrew G. APPLICANT: TSONIS, Con G. TITLE OF INVENTION: FUSION PROTEINS NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLGY & Lardner STREET: 3000 K Street, N.W.
CITY: Washington, D.C. CONDUTRY: USA COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: BP PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: IBM PC Compatible COMPUTER: BP PC COMPUTER: IBM PC COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 96.3%; Score 52; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE: protein US-07-690-983D-32
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SEQUENCE CHARACTERISTICS
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US-07-690-983D-37
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                                                                                                                                                       Query Match

96.3%; Score 52; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0025;

Matches 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             US-07-690-983D-8

Sequence 8, Application US/07690983D

Patent No. 5403586

GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, Gregory J. APPLICANT: STEWRET, Andrew G. APPLICANT: STEWRET, Andrew G. TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 47
CORRESPONDENCES: 1000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC COMPATIBLE OF STEMS: DOS COMPATES: PATENT SAFETH RELORDY DATA:
APPLICATION NUMBER: US/07/690,983D
FILING DATE: 25-JUN-1991
CLASSIPICATION NUMBER: PCT/AU90/00373
FILING DATE: 24-AUG-1990
ATPORTEY AREAL INFORMATION:
APPLICATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 19,768
REGISTRATION NUMBER: 19,768
REGISTRATION NUMBER: 19,768
REGISTRATION NUMBER: 19,768
REGISTRATION NUMBER: 10,708/148 CHAC
TELECOMMUNICATION INFORMATION:
NAME: BERNT STEPPING
                                                 LOCATION: 10
; COTHER INFORMATION: /note= "Represents glycinamide"
US-07-690-983D-7
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COTHER INFORMATION: /note= "Represents glycinamide"
US-07-690-983D-8
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                      FEATURE:
NAME/KEY: Modified-site
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INFORWATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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  MOLECULE TYPE: protein
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Sequence 7, Application US/07690983D
Sequence 7, Application US/07690983D
Patent No. 540386
GENERAL INFORMATION:
APPLICANT: STEWART, Andrew G.
APPLICANT: TSONIS, Con G.
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PREPLICATION NUMBER: US/07/690,983D
FILING DATE: 25-UN-1991
CLASSIFICATION NUMBER: US/07/690,983D
FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A.
REGISTRATION NUMBER: 16786/148 CHAC
TELERPHONE: (202)672-5309
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: unino acids
TYPER: unino acids
TYPER: unino acids
TYPER: unino acids
TYPER: unino acids
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CTHER INFORMATION: /note= "Represents glycinamide"
US-07-690-983D-6
FILING DATE: 25-JUN-1991
CLASSIFICATION: 435
RIOR APPLICATION DATA:
REPLICATION NUMBER: PCT/AU90/00373
FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Steephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/148 CHAC
TELEPHONE: (202)672-5300
TELEPRAN: (202)672-5309
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TYPE: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                         MIGNE:
NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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Ouery Match 96.3%; Score 52; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0025; Matches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: CONDU-5109
COMPUTER: PEADABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTER: PERTON: PC-DOS/MS-DOS
SOFTWARE: PERTON: PC-DOS/MS-DOS
SOFTWARE: PERTON DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/690,983D
FILING DATE: 24-AUG-1991
CLASSIFICATION 435
PRIOR APPLICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION UNMBER: 29.768
FILING DATE: 24-AUG-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
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LOCATION: 1
LOTHER INFORMATION: /note= "Represents pyroglutamic
OTHER INFORMATION: acid"
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OTHER INFORMATION: /note= "Represents glycinamide"
US-07-690-983D-1
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                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/07690983D
Patent No. 5403586
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, Gregory J.
APPLICANT: TSONIS, Con G.
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
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TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECTLE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
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Best Local Similarity 100.
Matches 8; Conservative
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US-07-690-983D-2

RESULT 6

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Sequence 2. Application Us/0763033D
Pasent No. 1843586:
APPLICANT: STRANKY, Addrew G.
PAPELLONY: STRANKY, Addrew G.
APPLICANT: STRANKY, Addrew G.
APPLICANT: STRANKY, Addrew G.
APPLICANT: STRANKY, Addrew G.
APPLICANT: STRANKY, Addrew G.
APPLICANT: STRANKY, Addrew G.
APPLICANT: STRANKY, Addrew G.
APPLICANT: STRANKY, Addrew G.
CONTINENT: BAD FOR SEQUENCES: A G.
CONTINENT: BAD FOR STREET, N. N.
CONTINENT: BAD FOR SEQUENCES: A G.
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CONTINENT: BAT A G.
CONTINENT: B
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Sequence 1, Application US/07983111

Patent No. 2584657

GENERAL INPORMATION:
APPLICANT: Fu Lu, Mun-Ying
APPLICANT: Fu Lu, Mun-Ying
APPLICANT: Fu Lu, Mun-Ying
APPLICANT: Reliand Thomas L.

TITLE OF INVENTION: "Compositions and Methods for the
TITLE OF INVENTION: Sublingual or Succal Administration of Therapeutic Applicants Applicants Applicants Applicants Applicants Applicants Applicants Applicants Applicants Applicants Applicated Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application Application App
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                                                                                                                                                                                                                                                                                                                                                                    Score 52; DB 1
Pred. No. 0.00
0; Mismatches
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Best Local Similarity 100.0%; P.
Matches 8; Conservative 0;
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NAME/KEY: Modified-site
COCATION: 10
OTHER INFORMATION: 91vote
US-07-983-111-1
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LOCATION: 1
OTHER INFORMATION: /note
OTHER INFORMATION: 5-0x0
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                                                                                                      LENGTH: 10 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                         ropology: linear molecule TYPE: protein US-07-714-540-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: Siz
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| Sequence 9, Application US/07714540
| Patent No. 526251
| GENERAL INFORMATION
| APPLICANT: Almquist, Ronald G. APPLICANT: Almquist, Ronald G. APPLICANT: Toll, Lawrence
| TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF ITILE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF INTEREST: Tell & Manella STREET: 545 Middlefield Road, Suite 200
| CITY: Menlo Park STATE: California COUNTRY: USA CONTRY: USA CONTRY: USA CONTRY: USA COMPUTER READABLE FORM: MEDIU TYPE: Floppy disk NEDIU TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Datentin Release #1.0, Version #1.25
| CURRENT APPLICATION DATA: PC-DOS/MS-DOS SOFTWARE: Datentin Release #1.0, Version #1.25
| CURRENT ANDROMENT TANDAMMENTON: S100 PELLING DATE: 19910607
| CLASSIFICATION NUMBER: US/07/714,540 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: HANDAMMENTON: S100 PELLING DATE: 
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OTHER INFORMATION: /product= "OTHER"

/note= "The Xaa at position 1 = pyroglutamic acid."

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRIT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-May-2000
CLASSIFICATION: JUNNOWN>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
NAME: SAZE: BETHAND BY
REGISTRATION NUMBER: 28 665
REPERENCE/DOCKET NUMBER: 18733/584/IMIN
TELLERAXION INFORMATION:
TELLERAXI: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.3%; Score 52; DB 1; Length 10; 100.0%; Pred. No. 0.0025; cive 0; Mismatches 0; Indels
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ATTORNEY/AGENT INFORMATION:
NAME: Reed, Diamne E.
REGISTRATION NUMBER: 31,292
REFERENCE/DOCKET NUMBER: 8500
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31,292
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 8; Conservative
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Sequence Sequence Sequence

Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Seq

Appli Appli

116, 2, Ap

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GENERAL GALY L.
GALY L.
TITLE OF INVENTION: RADIOMETAL-BINDING ANALOGUES OF
LEUTENIZING HORMONE RELEASING HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100.0%; Pred. No. 3e+05; B 4; Length 9; Similarity 100.0%; Pred. No. 3e+05; 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
US-08-453-588-22
US-08-188-223-1
US-08-188-223-3
US-08-406-935-5
US-08-406-935-5
US-08-474-555-1
US-08-474-555-1
US-08-474-555-1
US-08-474-692-1
US-08-245-678D-1
US-08-245-678D-1
US-08-694-865-2
US-08-684-865-2
US-08-488-1
                                                                                                                                                                           US-08-447-175A-6
US-08-747-137-116
US-08-878-748-2
                                                                                                                                                                                                                                                                                          Sequence 29, Application US/09890650
; Satent No. 6685947
; GENERAL INFORMATION:
APPLICANT: JACKSON, DAVID CHARLES
APPLICANT: GOURAVI, GHOSH
TITLE OF INVENTION: THELPER CELL EPITOPES
FILE REFERENCE: 47-152
CURRENT APPLICATION NUMBER: US/09/890,650
CURRENT APPLICATION NUMBER: US/09/890,650
SUMMER OF SEQ ID NOS: 30
SEQ ID NOS: 30
SEQ ID NO 29
                                                                                                                                                                                                                                    ALIGNMENTS
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US-09-572-339-1
Sequence 1, Application US/09572339
Sequence No. RE37710
GENERAL INFORMATION:
APPLICANT: MCBRIDE, William J.
APPLICANT: MCBRIDE, Habibe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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; ORGANISM: Canis sp.
US-09-890-650-29
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   RESULT 1
US-09-890-650-29
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Sequence 4, A
Sequence 6, A
Sequence 8, A
Sequence 10,
Sequence 12,
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Sequence 7,
Sequence 8,
Sequence 32
Sequence 37,
Sequence 1,
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Sequence 1
Sequence 1
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                   GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-572-339-1

US-07-983-11-11

US-07-983-11-11

US-07-690-983D-2

US-07-690-983D-6

US-07-690-983D-6

US-07-690-983D-6

US-07-690-983D-8

US-07-690-983D-8

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US-07-690-983D-8

US-07-690-983D-8

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US-08-453-588-14
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                sw model
                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                               protein search, using
                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                   US-09-848-834A-1
54
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                Perfect score:
                                                                                                                                                                                   Scoring table:
                                                                  OM protein
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                                                                                                                                                              Sequence:
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Gaps

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Length 10;

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Query Match 96.3%; Score 52; DB 9;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 8; Conservative 0; Mismatches 0
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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CRGANISM: Porcine
US-09-964-201A-32
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ORGANISM: Porcine
                                                                                                                                                                                                                                        US-09-964-201A-28
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0
                                                                                                    FARTHER INFORMATION: Description of Artificial Sequence: Gonadotrophin OTHER INFORMATION: Release Hormone Analogue NAME/KEY: MOD_RES
LOCATION: (1)
COTHER INFORMATION: CARBOXYLIC ACID
NAME/KEY: MOD RES
COTHER INFORMATION: CARBOXYLIC ACID
NAME/KEY: MOD RES
LOCATION: (10)
COTHER INFORMATION: And at position 10 is ethylamide;;
PUBLICATION INFORMATION:
PATENT PILING DATE: 1993-07-07
PUBLICATION DATE: 1993-07-07
PUBLICATION INFORMATION:
AUTHORS: Rousselle, Christophe
JOORNAL: MOL Pharmacol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Gonadotrophin OTHER INFORMATION: Release Hormone Analogue
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Xaa at position 1 is PyroGlu; PYRROLIDONE
OTHER INFORMATION: CARBOXVIIC ACID
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: Xaa at position 10 is Aza-Gly-NH2;
PUBLICATION INFORMATION:
PATENT FILING DATE: 1993-07-07
PUBLICATION DATE: 1993-07-07
PUBLICATION DATE: 1997-05-20
PUBLICATION DATE: 1997-05-20
PUBLICATION INFORMATION:
JOURNAL: Mol. Pharmacol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4. Application US/09810601

Patent No. US2002017545A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Composorions and Methods for Treating Gonadotrophin TITLE OF INVENTION: Related Illnesses
TITLE OF INVENTION: Related Illnesses
CURRENT APPLICATION NUMBER: US/09/810,601
CURRENT FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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SEQ ID NO 3
LENGTH: 10
TYPE: PRT
ORCANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Conservative
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Best Local Similarity
Matches 8; Conserv
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DATE: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGES: 679-686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28, Application US/09964201A
| Sequence 28, Application No. US2030091575A1
| GENERAL INFORMATION |
| APPLICANT: Kenten, John H |
| APPLICANT: Tramontano, Alfonso |
| APPLICANT: Pilon, Aprile L |
| APPLICANT: Roberts, Serven.F |
| TILE OF INVENTION HEAT-SHOCK FUSION-BASED VACCINE SYSTEM |
| TILE OF INVENTION NUMBER: US,09964,201A |
| CURRENT APPLICANTON NUMBER: US,09964,201A |
| CURRENT PILING DATE: 2002-05-21 |
| NUMBER OF SEQ ID NOS: 35 |
| SEQ ID NOS: 35 |
| SEQ ID NOS: 35 |
| SEQ ID NOS: 36 |
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| Publication No. US20030091575A1
| GENERAL INPORMATION:
| APPLICANT: Kenten, John H
| APPLICANT: Tramontano, Alfonso
| APPLICANT: Ichnas, Gerald L
| APPLICANT: Pilon, Aprile L
| APPLICANT: Roberts, Gerven F
| TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
| FILE REFERENCE: US. Patent Application No. US20030091575A1 09\026,276
| CURRENT PILING DATE: 2002-05-21
| NUMBER OF SEQ ID NOS: 35
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 32
| LENGTH: 10
| LENGTH: 10
Gaps
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0; Mismatches
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TYPE: PRT
ORGANISM: Artificial Sequence
NUMBER OF SEQUENCES: 41
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       Sequence 1, Application US/09305924A
Publication No. US20030091579A1
GENERAL INFORMATION:
APPLICANT: Jack G. Manns
APPLICANT: Stephen D. Acres
APPLICANT: Stephen D. Acres
APPLICANT: Richard Harland
TITLE OF INVENTION: WENTHODS OF RAISING ANIMALS FOR MEAT PRODUCTION
FILE REFERENCE: 9001-0048
CURRENT APPLICATION NUMBER: US/09/305,924A
CURRENT FILING DATE: 1999-05-05
BARLIER APPLICATION NUMBER: US 60/084,217
BARLIER PILING DATE: 1998-05-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 10
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| Sequence 9, Application US/09305924A
| Publication No. US20030091579A1
| GENERAL INFORMATION:
| APPLICANT: Stephen D. Acres
| APPLICANT: Stephen D. Acres
| APPLICANT: Stephen D. Acres
| APPLICANT: Stephen D. Acres
| PILE REPERENCE: 9001-0048
| TITLE OF INVENTION: WHETHOUS OF RAISING ANIMALS FOR MEAT PRODUCTION
| FILE REPERENCE: 9001-0048
| CURRENT APPLICATION NUMBER: US/09/305,924A
| CURRENT PILING DATE: 1999-05-05
| EARLIER APPLICATION UNMBER: US 60/084,217
| EARLIER PILING DATE: 1998-05-05
| NUMBER OF SEQ ID NOS: 14
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 9
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Publication No. US20020165159A1
GENERAL INPORMATION:
APPLICANT: WcCann, Samuel M.
Yu, Wen H.
TITLE OF INVENTION: FSH-Releasing Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MOD_RES

1 LOCATION: (1)

2 OTHER INFORMATION: Xaa is pyroglutamic acid
US-09-305-924-1
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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; ORGANISM: GDRH
US-09-305-924-9
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ORGANISM: GNRH
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US-10-109-331-2
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US-09-305-924-1
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